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Patentanmeldung Nr. | Patent application No. | Demande de brevet n°

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Im Auftrag

For the President of the European Patent Office

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Methods and nucleic acids for the analysis of CpG dinucleotide methylation status associated with the development of prostate cancer

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METHODS AND NUCLEIC ACIDS FOR THE ANALYSIS OF CpG DINUCLEOTIDE METHYLATION STATUS ASSOCIATED WITH THE DEVELOPMENT OF PROSTATE CANCER.

FIELD OF THE INVENTION

The present invention relates to human DNA sequences that exhibit altered methylation patterns (hypermethylation or hypomethylation) in cancer patients. Particular embodiments of the invention provide highly accurate methods for detection and differentiation of prostate carcinomas.

BACKGROUND

Correlation of aberrant DNA methylation with cancer. Aberrant DNA methylation within CpG 'islands' is characterized by *hyper-* or *hypomethylation* of CpG dinucleotide sequences leading to abrogation or overexpression of a broad spectrum of genes, and is among the earliest and most common alterations found in, and correlated with human malignancies. Additionally, abnormal methylation has been shown to occur in CpG-rich regulatory elements in intronic and coding parts of genes for certain tumors. In colon cancer, aberrant DNA methylation constitutes one of the most prominent alterations and inactivates many tumor suppressor genes including, *inter alia*, p14ARF, p16INK4a, THBS1, MINT2, and MINT31 and DNA mismatch repair genes such as hMLH1.

Aside from the specific hypermethylation of tumor suppressor genes, an overall hypomethylation of DNA can be observed in tumor cells. This decrease in global methylation can be detected early, far before the development of frank tumor formation. A correlation between hypomethylation and increased gene expression has been determined for many oncogenes.

Prostate cancer. The prostate is a male sex accessory gland, comprising about 30 to 50 branched glands. It is surrounded by a fibroelastic capsule that separates the gland into discrete lobes. The *central* zone of the organ is composed of pseudo stratified epithelium, the *peripheral* zone comprises the bulk of the organ and the two tissue types are separated by a *transitional* zone.

Benign prostate hypertrophy is present in about 50% of men aged 50 or above, and in 95% of men aged 75 or above. Prostate

cancer is a significant health care problem in Western countries with an incidence of 180 per 100,000 in the United States in 1999 (*Cancer J. Clin.*, 49:8, 1999).

Diagnosis and prognosis of prostate cancer; deficiencies of prior art approaches. Different screening strategies have been employed with at least some degree of success to improve early detection of prostate cancer, including determination of levels of prostate specific antigen ("PSA") and digital rectal examination. If a prostate carcinoma is suspected in a patient, diagnosis of cancer is confirmed or excluded by the histological and cytological analysis of biopsy samples for features associated with malignant transformation. The *zone of origin* of a prostatic cell proliferative disorder is currently determined by the 'PSA density.' PSA density is determined by dividing the weight of the prostate (as estimated by transrectal ultrasound) by the prostate specific antigen levels of the patient. Levels of over 15% percent are considered as indicative of prostate cancer and grounds for a biopsy. The biopsy, in turn, is used for histological and cytological analysis to determine the *zone of origin*.

However, using routine histological examination, it is often difficult to distinguish benign hyperplasia of the prostate from early stages of prostate carcinoma, even if an adequate biopsy is obtained (McNeal J. E. et al., *Hum. Pathol.* 2001, 32:441-6). Furthermore, small or otherwise insufficient biopsy samples often impede the analysis.

Molecular markers would offer the advantage that they could be used to efficiently analyze even very small tissue samples, and samples whose tissue architecture has not been maintained. Within the last decade, numerous genes have been studied with respect to differential expression among benign hyperplasia of the prostate and different grades of prostate cancer.

However, no single marker has as yet been shown to be sufficient for the diagnosis of prostate tumors in a clinical setting..

Alternatively, high-dimensional mRNA based approaches may, in particular instances, provide a means to distinguish between different tumor types and benign and malignant lesions. However, application of such approaches as a routine diagnostic

tool in a clinical environment is impeded and substantially limited by the extreme instability of mRNA, the rapidly occurring expression changes following certain triggers (*e.g.*, sample collection), and, most importantly, by the large amount of mRNA needed for analysis which often cannot be obtained from a routine biopsy (see, *e.g.*, Lipshutz, R. J. et al., *Nature Genetics* 21:20-24, 1999; Bowtell, D. D. L. *Nature Genetics Suppl.* 21:25-32, 1999).

The GSTP1 gene. The core promoter region of the Gluthione S-Transferase P gene (GSTP1; accession no. NM_000852) has been shown to be hypermethylated in prostate tumor tissue. The glutathione S-transferase pi enzyme is involved in the detoxification of electrophilic carcinogens, and impaired or decreased levels of enzymatic activity (GSTPi impairment) have been associated with the development of neoplasms, particularly in the prostate. Mechanisms of GSTPi impairment include mutation (the GSTP*B allele has been associated with a higher risk of cancer) and methylation.

Prior art GSTP1 studies. Lee et al., in United States Patent No 5,552,277, disclosed that the expression of the gluthione-S-transferase (GST) Pi gene was downregulated in a significant proportion of prostate carcinomas. Moreover, by means of restriction enzyme analysis they were able to show that the promoter region of the of the GSTPi gene was upmethylated (hypermethylated) in prostate carcinomas as opposed to normal prostate and leukocyte tissue. However, due to the limited and imprecise nature of the analysis technique used (HpaIII digestion, followed by Southern blotting) the exact number and position of the methylated CG dinucleotides were not characterized.

Douglas et al. (WO9955905) used a method comprising bisulfite treatment, followed by methylation specific PCR to show that prostate carcinoma-specific GSTPi hypermethylation was localized to the core promoter regions, and localized a number of CpG positions that had not been characterised by Lee et al.

Herman and Baylin (United States Patent No. 6,017,704) describe the use of methylation specific primers for methylation analysis, and describe a particular primer pair

suitable for the analysis of the corresponding methylated GSTPi promoter sequence.

However, with respect to the use of GSTPi markers, the prior art is limited with respect to the number of GSTPi promoter CpG sequences that have been characterized for differential methylation status. Moreover, there are no disclosures, suggestions or teachings in the prior art of how such markers could be used to distinguish among benign hyperplasia of the prostate and different grades of prostate cancer.

Aberrant genetic methylation has also been observed in several other genes including AR, p16 (CDKN2a/INK4a), CD44, CDH1. Genome wide hypomethylation for example of the LINE-1 repetitive element has also been associated with tumor progression (Santourlidis S ,Florl A ,Ackermann R ,Wirtz HC ,Schulz WA 'High frequency of alterations in DNA methylation in adenocarcinoma of the prostate.' Prostate 1999 May 15;39(3):166-74).

However, use of these genes as alternative or supplemental diagnostic, or otherwise clinically useful markers in a commercial setting has not been enabled. The application of differentially methylated genes to clinically utilizable platforms requires much further investigation into the sensitivity and specificity of the genes. For example, in the case of the gene CD44, a known metastasis suppressor, downregulation was associated with hypermethylation. However the use of this gene as a commercially avalable marker was not enabled as it was also methylated in normal tissues. See Vis AN Oomen M Schroder FH van der Kwast TH 'Feasibility of assessment of promoter methylation of the CD44 gene in serum of prostate cancer patients.' Mol Urol. 2001 Winter;5(4):199-203.

Development of medical tests. Two key evaluative measures of any medical screening or diagnostic test are its sensitivity and specificity, which measure how well the test performs to accurately detect all affected individuals without exception, and without falsely including individuals who do not have the target disease (predictive value). Historically, many diagnostic tests have been criticized due to poor sensitivity and specificity.

A true positive (TP) result is where the test is positive and the condition is present. A false positive (FP) result is where the test is positive but the condition is not present. A true negative (TN) result is where the test is negative and the condition is not present. A false negative (FN) result is where the test is negative but the condition is not present.

Sensitivity = TP/(TP+FN)
Specificity = TN/(FP+TN)
Predictive value = TP/(TP+FP)

Sensitivity is a measure of a test's ability to correctly detect the target disease in an individual being tested. A test having poor sensitivity produces a high rate of false negatives, i.e., individuals who have the disease but are falsely identified as being free of that particular disease. The potential danger of a false negative is that the diseased individual will remain undiagnosed and untreated for some period of time, during which the disease may progress to a later stage wherein treatments, if any, may be less effective. An example of a test that has low sensitivity is a protein-based blood test for HIV. This type of test exhibits poor sensitivity because it fails to detect the presence of the virus until the disease is well established and the virus has invaded the bloodstream in substantial numbers. In contrast, an example of a test that has high sensitivity is viral-load detection using the polymerase chain reaction (PCR). High sensitivity is achieved because this type of test can detect very small quantities of the virus. High sensitivity is particularly important when the consequences of missing a diagnosis are high.

Specificity, on the other hand, is a measure of a test's ability to identify accurately patients who are free of the disease state. A test having poor specificity produces a high rate of false positives, i.e., individuals who are falsely identified as having the disease. A drawback of false positives is that they force patients to undergo unnecessary medical procedures treatments with their attendant risks, emotional and

financial stresses, and which could have adverse effects on the patient's health. A feature of diseases which makes it difficult to develop diagnostic tests with high specificity is that disease mechanisms, particularly in cancer, often involve a plurality of genes and proteins. Additionally, certain proteins may be elevated for reasons unrelated to a disease state. An example of a test that has high specificity is a gene-based test that can detect a p53 mutation. Specificity is important when the cost or risk associated with further diagnostic procedures or further medical intervention are very high.

The PSA blood test has a sensitivity of 73%, specificity of 60% and predictive value of 31.5%. PSA sensitivity and specificity can be improved but involve tradeoffs. PSA sensitivity can be improved by adjusting the "normal" PSA level to a lower value for younger men or by following serum PSA values in an individual patient over time (PSA velocity). Both methods will increase the number of cancers detected, but they also increase the number of men undergoing biopsy. Conversely, specificity can be improved by using higher "normal" PSA levels for older men, by using the free-to-total PSA ratio, or by adjusting the normal value according to the size of the prostate. These three methods decrease the number of unnecessary biopsies, but they increase the risk that some cancers will be missed.
It can therefore be seen that there exists a need for a means of prostate cancer diagnosis with improved sensitivity, specificity and/or predictive value.

Sensitivity and specificity of quantitative methylation-specific polymerase chain reaction (QMSP) assay alone (without histological analysis) in prostate cancer analysis of needle biopsies has ranged from 30% sensitivity and 100% specificity to 89% sensitivity and 64% specificity (Harden *et. al.* J Natl Cancer Inst 2003; 95: 1634-1637). However the predictive value of said technique as a clinical screening tool was not analysed. Furthermore, genetic testing of serum and bodily fluids such as urine and saliva would reduce the need for biopsies to detect cancer and would thus be the most effective screening or monitering tool. However the development of such tests requires an extremely high degree of sensitivity

and specificity. Analysis of GSTPi gene hypermethylation (Cairns P, Esteller M, Herman JG, Schoenberg M, Jeronimo C, Sanchez-Cespedes M, et al. Molecular detection of prostate cancer in urine by GSTP1 hypermethylation. Clin Cancer Res 2001;7:2727-30.) in urine sediment of prostate cancer patients showed that only 6 out of 22 individuals with elevated methylation levels in biopsied tumors showed corresponding hypermethylation in urine samples.

Multifactorial approach. Cancer diagnostics has traditionally relied upon the detection of single molecular markers (e.g. gene mutations, elevated PSA levels). Unfortunately, cancer is a disease state in which single markers have typically failed to detect or differentiate many forms of the disease. Thus, assays that recognize only a single marker have been shown to be of limited predictive value. A fundamental aspect of this invention is that methylation based cancer diagnostics and the screening, diagnosis, and therapeutic monitoring of such diseases will provide significant improvements over the state-of-the-art that uses single marker analyses by the use of a selection of multiple markers. The multiplexed analytical approach is particularly well suited for cancer diagnostics since cancer is not a simple disease, this multi-factorial "panel" approach is consistent with the heterogeneous nature of cancer, both cytologically and clinically.

Key to the successful implementation of a panel approach to methylation based diagnostic tests is the design and development of optimized panels of markers that can characterize and distinguish disease states. This patent application describes an efficient and unique panel of genes the methylation analysis of one or a combination of the members of the panel enabling the detection of cell proliferative disorders of the prostate with a particularly high sensitivity, specificity and/or predictive value.

Pronounced need in the art. Therefore, in view of the incidence of prostate hyperplasia (50% of men aged 50 or above, and 95% of men aged 75 or above) and prostate cancer (180 per 100,000), there is a substantial need in the art for the development of molecular markers that could be used to

effectively distinguish among benign hyperplasia of the prostate and different grades of prostate cancer. Additionally, there is a pronounced need in the art for the development of molecular markers that could be used to provide sensitive, accurate and non-invasive methods (as opposed to, e.g., biopsy and transrectal ultrasound) for the diagnosis, prognosis and treatment of prostate cell proliferative disorders.

SUMMARY OF THE INVENTION

The disclosed invention provides a means for detection of or differentiation between prostate cell proliferative disorders by analysis of a gene panel, with a sensitivity and specificity suitable for use in a body fluid or serum assay. The present invention provides novel methods for detecting or distinguishing between prostate cell proliferative disorders with a sensitivity of greater than 30% and a specificity of greater than 65%. Said method is most preferably utilised for detecting or detecting and distinguishing between prostate cell proliferative disorders. The invention provides a method for the analysis of biological samples for features associated with the development of prostate cell proliferative disorders, the method characterised in that at least one nucleic acid, or a fragment thereof, from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 20 is/are contacted with a reagent or series of reagents capable of distinguishing between methylated and non methylated CpG dinucleotides within the genomic sequence, or sequences of interest.

The present invention provides a method for ascertaining genetic and/or epigenetic parameters of genomic DNA. The method has utility for the improved diagnosis, treatment and monitoring of prostate cell proliferative disorders, more specifically by enabling the improved identification of and differentiation between subclasses of said disorder and the genetic predisposition to said disorders. The invention presents improvements over the state of the art in that it enables a more specific and sensitive classification of prostate cell proliferative disorders than that achieved by

currently used tests thereby allowing for improved and informed treatment of patients.

Preferably, the source of the test sample is selected from the group consisting of cells or cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof. Preferably, the source is biopsies, bodily fluids, ejaculate, urine, or blood.

Specifically, the present invention provides a method for detecting prostate cell proliferative disorders with a sensitivity of greater than 30% and a specificity of greater than 65%, comprising: obtaining a biological sample comprising genomic nucleic acid(s); contacting the nucleic acid(s), or a fragment thereof, with one reagent or a plurality of reagents sufficient for distinguishing between methylated and non methylated CpG dinucleotide sequences within a target sequence of the subject nucleic acid, wherein the target sequence comprises, or hybridizes under stringent conditions to, a sequence comprising at least 16 contiguous nucleotides of SEQ ID NO: 1 to 20, said contiguous nucleotides comprising at least one CpG dinucleotide sequence; and determining, based at least in part on said distinguishing, the methylation state of at least one target CpG dinucleotide sequence, or an average, or a value reflecting an average methylation state of a plurality of target CpG dinucleotide sequences. Preferably, distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises methylation state-dependent conversion or non-conversion of at least one such CpG dinucleotide sequence to the corresponding converted or non-converted dinucleotide sequence within a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO: 20, and contiguous regions thereof corresponding to the target sequence.

Additional embodiments provide a method for the detection of prostate cell proliferative disorders with a sensitivity of greater than 30% and a specificity of greater than 65%, comprising: obtaining a biological sample having subject genomic DNA; extracting the genomic DNA; treating the genomic DNA, or a fragment thereof, with one or more reagents to convert 5-position unmethylated cytosine bases to uracil or to another base that is detectably dissimilar to cytosine in terms

of hybridization properties; contacting the treated genomic DNA, or the treated fragment thereof, with an amplification enzyme and at least two primers comprising, in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting SEQ ID NO: 5 to SEQ ID NO: 20, and complements thereof, wherein the treated DNA or the fragment thereof is either amplified to produce an amplificate, or is not amplified; and determining, based on a presence or absence of, or on a property of said amplificate, the methylation state of at least one CpG dinucleotide sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 4 , or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotide sequences thereof. Preferably, at least one such hybridizing nucleic acid molecule or peptide nucleic acid molecule is bound to a solid phase. Preferably, determining comprises use of at least two methods selected from the group consisting of: hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO: 20, and complements thereof; hybridizing at least one nucleic acid molecule, bound to a solid phase, comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO: 20, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO: 20, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing of the amplificate.

14 14 Additional embodiments provide novel genomic and chemically modified nucleic acid sequences, as well as oligonucleotides and/or PNA-oligomers for analysis of cytosine

methylation patterns within sequences from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 4 .

BRIEF DESCRIPTION OF THE DRAWINGS

DETAILED DESCRIPTION OF THE INVENTION

Definitions:

The term "Observed/Expected Ratio" ("O/E Ratio") refers to the frequency of CpG dinucleotides within a particular DNA sequence, and corresponds to the [number of CpG sites / (number of C bases x number of G bases)] x band length for each fragment.

The term "CpG island" refers to a contiguous region of genomic DNA that satisfies the criteria of (1) having a frequency of CpG dinucleotides corresponding to an "Observed/Expected Ratio" >0.6, and (2) having a "GC Content" >0.5. CpG islands are typically, but not always, between about 0.2 to about 1 kb in length.

The term "methylation state" or "methylation status" refers to the presence or absence of 5-methylcytosine ("5-mCyt") at one or a plurality of CpG dinucleotides within a DNA sequence. Methylation states at one or more particular palindromic CpG methylation sites (each having two CpG CpG dinucleotide sequences) within a DNA sequence include "unmethylated," "fully-methylated" and "hemi-methylated."

The term "hemi-methylation" or "hemimethylation" refers to the methylation state of a palindromic CpG methylation site, where only a single cytosine in one of the two CpG dinucleotide sequences of the palindromic CpG methylation site is methylated (*e.g.*, 5'-CC^{M}GG-3' (top strand): 3'-GGCC-5' (bottom strand)).

The term "hypermethylation" refers to the average methylation state corresponding to an *increased* presence of 5-mCyt at one or a plurality of CpG dinucleotides within a DNA sequence of a test DNA sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

The term "hypomethylation" refers to the average methylation state corresponding to a *decreased* presence of 5-mCyt at one or a plurality of CpG dinucleotides within a DNA sequence of a

test DNA sample, relative to the amount of 5-mCyt found at corresponding CpG dinucleotides within a normal control DNA sample.

The term "microarray" refers broadly to both "DNA microarrays," and 'DNA chip(s),' as recognized in the art, encompasses all art-recognized solid supports, and encompasses all methods for affixing nucleic acid molecules thereto or synthesis of nucleic acids thereon.

"Genetic parameters" are mutations and polymorphisms of genes and sequences further required for their regulation. To be designated as mutations are, in particular, insertions, deletions, point mutations, inversions and polymorphisms and, particularly preferred, SNPs (single nucleotide polymorphisms).

"Epigenetic parameters" are, in particular, cytosine methylations. Further epigenetic parameters include, for example, the acetylation of histones which, however, cannot be directly analyzed using the described method but which, in turn, correlate with the DNA methylation.

The term "bisulfite reagent" refers to a reagent comprising bisulfite, disulfite, hydrogen sulfite or combinations thereof, useful as disclosed herein to distinguish between methylated and unmethylated CpG dinucleotide sequences.

The term "Methylation assay" refers to any assay for determining the methylation state of one or more CpG dinucleotide sequences within a sequence of DNA.

The term "MS.AP-PCR" (Methylation-Sensitive Arbitrarily-Primed Polymerase Chain Reaction) refers to the art-recognized technology that allows for a global scan of the genome using CG-rich primers to focus on the regions most likely to contain CpG dinucleotides, and described by Gonzalgo et al., *Cancer Research* 57:594-599, 1997.

The term "MethyLight™" refers to the art-recognized fluorescence-based real-time PCR technique described by Eads et al., *Cancer Res.* 59:2302-2306, 1999.

The term "HeavyMethyl™" assay, in the embodiment thereof implemented herein, refers to a HeavyMethyl™ refer to the use of methylation specific *blocking* probes covering CpG positions between the amplification primers.

The term "Ms-SNuPE" (Methylation-sensitive Single Nucleotide Primer Extension) refers to the art-recognized assay described by Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997.

The term "MSP" (Methylation-specific PCR) refers to the art-recognized methylation assay described by Herman et al. *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996, and by US Patent No. 5,786,146.

The term "COBRA" (Combined Bisulfite Restriction Analysis) refers to the art-recognized methylation assay described by Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997.

The term "MCA" (Methylated CpG Island Amplification) refers to the methylation assay described by Toyota et al., *Cancer Res.* 59:2307-12, 1999, and in WO 00/26401A1.

The term "hybridization" is to be understood as a bond of an oligonucleotide to a complementary sequence along the lines of the Watson-Crick base pairings in the sample DNA, forming a duplex structure.

"Stringent hybridization conditions," as defined herein, involve hybridizing at 68°C in 5x SSC/5x Denhardt's solution/1.0% SDS, and washing in 0.2x SSC/0.1% SDS at room temperature, or involve the art-recognized equivalent thereof (e.g., conditions in which a hybridization is carried out at 60°C in 2.5 x SSC buffer, followed by several washing steps at 37°C in a low buffer concentration, and remains stable). Moderately stringent conditions, as defined herein, involve including washing in 3x SSC at 42°C, or the art-recognized equivalent thereof. The parameters of salt concentration and temperature can be varied to achieve the optimal level of identity between the probe and the target nucleic acid. Guidance regarding such conditions is available in the art, for example, by Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, N.Y.; and Ausubel et al. (eds.), 1995, Current Protocols in Molecular Biology, (John Wiley & Sons, N.Y.) at Unit 2.10.

The terms 'sensitivity' and 'specificity' refer to values calculated with reference to a sample set of male patients with an average age of 65 and a mixed ethnic range including caucasian and african american.

Overview:

The present invention provides for molecular genetic markers that have novel utility for the analysis of methylation patterns associated with the development of prostate cell proliferative disorders with a sensitivity of greater than 30% and a specificity of greater than 65%. Said markers may be used for detecting or distinguishing between prostate cell proliferative disorders, thereby providing improved means for the classification and treatment of said disorders. The markers according to the present invention are analysed in the form of a 'panel' wherein the methylation of one or more genetic sequences of the genes

Bisulfite modification of DNA is an art-recognized tool used to assess CpG methylation status. 5-methylcytosine is the most frequent covalent base modification in the DNA of eukaryotic cells. It plays a role, for example, in the regulation of the transcription, in genetic imprinting, and in tumorigenesis. Therefore, the identification of 5-methylcytosine as a component of genetic information is of considerable interest. However, 5-methylcytosine positions cannot be identified by sequencing, because 5-methylcytosine has the same base pairing behavior as cytosine. Moreover, the epigenetic information carried by 5-methylcytosine is completely lost during, *e.g.*, PCR amplification.

The most frequently used method for analyzing DNA for the presence of 5-methylcytosine is based upon the specific reaction of bisulfite with cytosine whereby, upon subsequent alkaline hydrolysis, cytosine is converted to uracil which corresponds to thymine in its base pairing behavior. Significantly, however, 5-methylcytosine remains unmodified under these conditions. Consequently, the original DNA is *converted* in such a manner that methylcytosine, which originally could not be distinguished from cytosine by its hybridization behavior, can now be detected as the only remaining cytosine using standard, art-recognized molecular biological techniques, for example, by amplification and hybridization, or by sequencing. All of these techniques are based on differential base pairing properties, which can now be fully exploited.

The prior art, in terms of sensitivity, is defined by a method comprising enclosing the DNA to be analyzed in an agarose matrix, thereby preventing the diffusion and renaturation of the DNA (bisulfite only reacts with single-stranded DNA), and replacing all precipitation and purification steps with fast dialysis (Olek A, et al., A modified and improved method for bisulfite based cytosine methylation analysis, *Nucleic Acids Res.* 24:5064-6, 1996). It is thus possible to analyze individual cells for methylation status, illustrating the utility and sensitivity of the method. An overview of art-recognized methods for detecting 5-methylcytosine is provided by Rein, T., et al., *Nucleic Acids Res.*, 26:2255, 1998.

The bisulfite technique, barring few exceptions (*e.g.*, Zeschnigk M, et al., *Eur J Hum Genet.* 5:94-98, 1997), is currently only used in research. In all instances, short, specific fragments of a known gene are amplified subsequent to a bisulfite treatment, and either completely sequenced (Olek & Walter, *Nat Genet.* 1997 17:275-6, 1997), subjected to one or more primer extension reactions (Gonzalgo & Jones, *Nucleic Acids Res.*, 25:2529-31, 1997; WO 95/00669; U.S. Patent No. 6,251,594) to analyze individual cytosine positions, or treated by enzymatic digestion (Xiong & Laird, *Nucleic Acids Res.*, 25:2532-4, 1997). Detection by hybridization has also been described in the art (Olek et al., WO 99/28498). Additionally, use of the bisulfite technique for methylation detection with respect to individual genes has been described (Grigg & Clark, *Bioessays*, 16:431-6, 1994; Zeschnigk M, et al., *Hum Mol Genet.*, 6:387-95, 1997; Feil R, et al., *Nucleic Acids Res.*, 22:695-, 1994; Martin V, et al., *Gene*, 157:261-4, 1995; WO 9746705 and WO 9515373).

The present invention provides for the use of the bisulfite technique , in combination with one or more methylation assays, for determination of the methylation status of CpG dinuclotide sequences within sequences from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 4 . According to the present invention, determination of the methylation status of CpG dinuclotide sequences within sequences from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 4 has diagnostic and prognostic utility.

Methylation Assay Procedures. Various methylation assay procedures are known in the art, and can be used in conjunction with the present invention. These assays allow for determination of the methylation state of one or a plurality of CpG dinucleotides (*e.g.*, CpG islands) within a DNA sequence. Such assays involve, among other techniques, DNA sequencing of bisulfite-treated DNA, PCR (for sequence-specific amplification), Southern blot analysis, and use of methylation-sensitive restriction enzymes.

For example, genomic sequencing has been simplified for analysis of DNA methylation patterns and 5-methylcytosine distribution by using bisulfite treatment (Frommer et al., *Proc. Natl. Acad. Sci. USA* 89:1827-1831, 1992). Additionally, restriction enzyme digestion of PCR products amplified from bisulfite-converted DNA is used, *e.g.*, the method described by Sadri & Hornsby (*Nucl. Acids Res.* 24:5058-5059, 1996), or COBRA (Combined Bisulfite Restriction Analysis) (Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997).

COBRA. COBRA analysis is a quantitative methylation assay useful for determining DNA methylation levels at specific gene loci in small amounts of genomic DNA (Xiong & Laird, *Nucleic Acids Res.* 25:2532-2534, 1997). Briefly, restriction enzyme digestion is used to reveal methylation-dependent sequence differences in PCR products of sodium bisulfite-treated DNA. Methylation-dependent sequence differences are first introduced into the genomic DNA by standard bisulfite treatment according to the procedure described by Frommer et al. (*Proc. Natl. Acad. Sci. USA* 89:1827-1831, 1992). PCR amplification of the bisulfite converted DNA is then performed using primers specific for the interested CpG islands, followed by restriction endonuclease digestion, gel electrophoresis, and detection using specific, labeled hybridization probes. Methylation levels in the original DNA sample are represented by the relative amounts of digested and undigested PCR product in a linearly quantitative fashion across a wide spectrum of DNA methylation levels. In addition, this technique can be reliably applied to DNA obtained from microdissected paraffin-embedded tissue samples. Typical reagents (*e.g.*, as might be found in a typical COBRA-based kit) for COBRA analysis may include, but are not limited to: PCR primers for specific gene

(or methylation-altered DNA sequence or CpG island); restriction enzyme and appropriate buffer; gene-hybridization oligo; control hybridization oligo; kinase labeling kit for oligo probe; and radioactive nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery reagents or kits (*e.g.*, precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

Preferably, assays such as "MethyLight•" (a fluorescence-based real-time PCR technique) (Eads et al., *Cancer Res.* 59:2302-2306, 1999), Ms-SNuPE (Methylation-sensitive Single Nucleotide Primer Extension) reactions (Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997), methylation-specific PCR ("MSP"; Herman et al., *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996; US Patent No. 5,786,146), and methylated CpG island amplification ("MCA"; Toyota et al., *Cancer Res.* 59:2307-12, 1999) are used alone or in combination with other of these methods.

MethyLight•. The MethyLight• assay is a high-throughput quantitative methylation assay that utilizes fluorescence-based real-time PCR (TaqMan••) technology that requires no further manipulations after the PCR step (Eads et al., *Cancer Res.* 59:2302-2306, 1999). Briefly, the MethyLight• process begins with a mixed sample of genomic DNA that is converted, in a sodium bisulfite reaction, to a mixed pool of methylation-dependent sequence differences according to standard procedures (the bisulfite process converts unmethylated cytosine residues to uracil). Fluorescence-based PCR is then performed either in an "unbiased" (with primers that do not overlap known CpG methylation sites) PCR reaction, or in a "biased" (with PCR primers that overlap known CpG dinucleotides) reaction. Sequence discrimination can occur either at the level of the amplification process or at the level of the fluorescence detection process, or both.

The MethyLight• assay may be used as a quantitative test for methylation patterns in the genomic DNA sample, wherein sequence discrimination occurs at the level of probe hybridization. In this quantitative version, the PCR reaction provides for unbiased amplification in the presence of a fluorescent probe that overlaps a particular putative

methylation site. An unbiased control for the amount of input DNA is provided by a reaction in which neither the primers, nor the probe overlie any CpG dinucleotides. Alternatively, a qualitative test for genomic methylation is achieved by probing of the biased PCR pool with either control oligonucleotides that do not "cover" known methylation sites (a fluorescence-based version of the "MSP" technique), or with oligonucleotides covering potential methylation sites.

The MethyLight• process can by used with a "TaqMan®" probe in the amplification process. For example, double-stranded genomic DNA is treated with sodium bisulfite and subjected to one of two sets of PCR reactions using TaqMan® probes; *e.g.*, with either biased primers and TaqMan® probe, or unbiased primers and TaqMan® probe. The TaqMan® probe is dual-labeled with fluorescent "reporter" and "quencher" molecules, and is designed to be specific for a relatively high GC content region so that it melts out at about 10°C higher temperature in the PCR cycle than the forward or reverse primers. This allows the TaqMan® probe to remain fully hybridized during the PCR annealing/extension step. As the Taq polymerase enzymatically synthesizes a new strand during PCR, it will eventually reach the annealed TaqMan® probe. The Taq polymerase 5' to 3' endonuclease activity will then displace the TaqMan® probe by digesting it to release the fluorescent reporter molecule for quantitative detection of its now unquenched signal using a real-time fluorescent detection system.

Typical reagents (*e.g.*, as might be found in a typical MethyLight•-based kit) for MethyLight• analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); TaqMan® probes; optimized PCR buffers and deoxynucleotides; and Taq polymerase.

Ms-SNuPE. The Ms-SNuPE technique is a quantitative method for assessing methylation differences at specific CpG sites based on bisulfite treatment of DNA, followed by single-nucleotide primer extension (Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997). Briefly, genomic DNA is reacted with sodium bisulfite to convert unmethylated cytosine to uracil while leaving 5-methylcytosine unchanged. Amplification of the desired target sequence is then performed using PCR primers

specific for bisulfite-converted DNA, and the resulting product is isolated and used as a template for methylation analysis at the CpG site(s) of interest. Small amounts of DNA can be analyzed (*e.g.*, microdissected pathology sections), and it avoids utilization of restriction enzymes for determining the methylation status at CpG sites.

Typical reagents (*e.g.*, as might be found in a typical Ms-SNuPE-based kit) for Ms-SNuPE analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); optimized PCR buffers and deoxynucleotides; gel extraction kit; positive control primers; Ms-SNuPE primers for specific gene; reaction buffer (for the Ms-SNuPE reaction); and radioactive nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery regents or kit (*e.g.*, precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

MSP. MSP (methylation-specific PCR) allows for assessing the methylation status of virtually any group of CpG sites within a CpG island, independent of the use of methylation-sensitive restriction enzymes (Herman et al. *Proc. Natl. Acad. Sci. USA* 93:9821-9826, 1996; US Patent No. 5,786,146). Briefly, DNA is modified by sodium bisulfite converting all unmethylated, but not methylated cytosines to uracil, and subsequently amplified with primers specific for methylated versus unmethylated DNA. MSP requires only small quantities of DNA, is sensitive to 0.1% methylated alleles of a given CpG island locus, and can be performed on DNA extracted from paraffin-embedded samples. Typical reagents (*e.g.*, as might be found in a typical MSP-based kit) for MSP analysis may include, but are not limited to: methylated and unmethylated PCR primers for specific gene (or methylation-altered DNA sequence or CpG island), optimized PCR buffers and deoxynucleotides, and specific probes.

MCA. The MCA technique is a method that can be used to screen for altered methylation patterns in genomic DNA, and to isolate specific sequences associated with these changes (Toyota et al., *Cancer Res.* 59:2307-12, 1999). Briefly, restriction enzymes with different sensitivities to cytosine methylation in their recognition sites are used to digest

genomic DNAs from primary tumors, cell lines, and normal tissues prior to arbitrarily primed PCR amplification. Fragments that show differential methylation are cloned and sequenced after resolving the PCR products on high-resolution polyacrylamide gels. The cloned fragments are then used as probes for Southern analysis to confirm differential methylation of these regions. Typical reagents (*e.g.*, as might be found in a typical MCA-based kit) for MCA analysis may include, but are not limited to: PCR primers for arbitrary priming Genomic DNA; PCR buffers and nucleotides, restriction enzymes and appropriate buffers; gene-hybridization oligos or probes; control hybridization oligos or probes.

HeavyMethyl. The HeavyMethyl techniques is a means for selectively amplifying methylated as opposed to non-methylated DNA (or vice versa). Blocker oligonucleotides specific to either methylated or unmenthylated versions of a bisulfite treated target sequence are hybridised to the treated nucleic acids. The sample is then enzymatically amplified, wherein the hybridisation of the blocker oligonucleotides hinders amplification of the nucleic acid strand to which it is bound. Typical reagents (*e.g.*, as might be found in a typical HeavyMethyl-based kit) for HeavyMethyl analysis may include, but are not limited to: methylated or unmethylated blocker oligonucleotides for specific gene (or methylation-altered DNA sequence or CpG island), optimized PCR buffers and deoxynucleotides, and specific probes and primers.

GENOMIC SEQUENCES ACCORDING TO SEQ ID NO: 1 to SEQ ID NO: 4 , AND TREATED VARIANTS THEREOF ACCORDING TO SEQ ID NO: 5 to SEQ ID NO: 20, WERE DETERMINED TO HAVE UTILITY FOR DETECTING OR DISTINGUISHING BETWEEN OR AMONG PROSTATE CELL PROLIFERATIVE DISORDERS. .

The present invention is based upon the analysis of methylation levels within one or more genes taken from the group consisting GSTP1, HISTONE H4, PROSTAGLANDIN E2 RECEPTOR and ORPHAN NUCLEAR RECEPTOR NR5A2 and their regulatory regions and sequences thereof according to Table 5.

Particular embodiments of the present invention provide a novel application of the analysis of methylation levels and/or patterns within said genes and/or sequences that enables a precise detection, characterisation and/or treatment of prostate cell proliferative disorders. Early detection of prostate cell proliferative disorders is directly linked with disease prognosis, and the disclosed method thereby enables the physician and patient to make better and more informed treatment decisions. The methods disclosed according to the invention enable the detection and characterisation of prostate cell proliferative disorders with improved sensitivity and/or specificity of with a sensitivity of greater than 30% and a specificity of greater than 65%.

FURTHER IMPROVEMENTS

The present invention provides novel uses for genomic sequences selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 4 . Additional embodiments provide modified variants of SEQ ID NO: 1 to SEQ ID NO: 4 , as well as oligonucleotides and/or PNA-oligomers for analysis of cytosine methylation patterns within SEQ ID NO: 1 to SEQ ID NO: 4 .

An objective of the invention comprises analysis of the methylation state of one or more CpG dinucleotides within at least one of the genomic sequences selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 4 and sequences complementary thereto.

The disclosed invention provides treated nucleic acids, derived from genomic SEQ ID NO: 1 to SEQ ID NO 4 , wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization. The genomic sequences in question may comprise one, or more, consecutive or random methylated CpG positions. Said treatment preferably comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof .In a preferred embodiment of the invention, the objective comprises analysis of a modified nucleic acid comprising a sequence of at least 16 contiguous nucleotide bases in length of a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO: 20, wherein said sequence comprises at least one CpG, TpA or CpA

dinucleotide and sequences complementary thereto. The sequences of SEQ ID NO: 5 to SEQ ID NO: 20 provide modified versions of the nucleic acid according to SEQ ID NO: 1 to SEQ ID NO: 4 , wherein the modification of each genomic sequence results in the synthesis of a nucleic acid having a sequence that is unique and distinct from said genomic sequence as follows. For each sense strand genomic DNA, e.g., SEQ ID NO:1, four converted versions are disclosed. A first version wherein "C"••"T," but "CpG" remains "CpG" (*i.e.*, corresponds to case where, for the genomic sequence, all "C" residues of CpG dinucleotide sequences are methylated and are thus not converted); a second version discloses the complement of the disclosed genomic DNA sequence (i.e. *anti*sense strand), wherein "C"••"T," but "CpG" remains "CpG" (*i.e.*, corresponds to case where, for all "C" residues of CpG dinucleotide sequences are methylated and are thus not converted). The 'upmethylated' converted sequences of SEQ ID NO: 1 to SEQ ID NO: 4 correspond to SEQ ID NO: 5 to SEQ ID NO: 12. A third chemically converted version of each genomic sequences is provided, wherein "C"••"T" for all "C" residues, including those of "CpG" dinucleotide sequences (*i.e.*, corresponds to case where, for the genomic sequences, all "C" residues of CpG dinucleotide sequences are unmethylated); a final chemically converted version of each sequence, discloses the complement of the disclosed genomic DNA sequence (i.e. *anti*sense strand), wherein "C"••"T" for all "C" residues, including those of "CpG" dinucleotide sequences (*i.e.*, corresponds to case where, for the complement (*anti*sense strand) of each genomic sequence, all "C" residues of CpG dinucleotide sequences are unmethylated). The 'downmethylated' converted sequences of SEQ ID NO: 1 to SEQ ID NO: 4 correspond to SEQ ID NO: 13 to SEQ ID NO: 20.

120

In an alternative preferred embodiment, such analysis comprises the use of an oligonucleotide or oligomer for detecting the cytosine methylation state within genomic or pretreated (chemically modified) DNA, according to SEQ ID NO: 1 to SEQ ID NO: 20. Said oligonucleotide or oligomer comprising a nucleic acid sequence having a length of at least nine (9) nucleotides which hybridizes, under moderately stringent or stringent conditions (as defined herein above), to a pretreated

nucleic acid sequence according to SEQ ID NO: 5 to SEQ ID NO: 20 and/or sequences complementary thereto, or to a genomic sequence according to SEQ ID NO: 1 to SEQ ID NO: 4 and/or sequences complementary thereto.

Thus, the present invention includes nucleic acid molecules (*e.g.*, oligonucleotides and peptide nucleic acid (PNA) molecules (PNA-oligomers)) that hybridize under moderately stringent and/or stringent hybridization conditions to all or a portion of the sequences SEQ ID NO: 1 to SEQ ID NO: 20, or to the complements thereof. The hybridizing portion of the hybridizing nucleic acids is typically at least 9, 15, 20, 25, 30 or 35 nucleotides in length. However, longer molecules have inventive utility, and are thus within the scope of the present invention.

Preferably, the hybridizing portion of the inventive hybridizing nucleic acids is at least 95%, or at least 98%, or 100% identical to the sequence, or to a portion thereof of SEQ ID NO: 1 to SEQ ID NO: 20, or to the complements thereof.

Hybridizing nucleic acids of the type described herein can be used, for example, as a primer (*e.g.*, a PCR primer), or a diagnostic and/or prognostic probe or primer. Preferably, hybridization of the oligonucleotide probe to a nucleic acid sample is performed under stringent conditions and the probe is 100% identical to the target sequence. Nucleic acid duplex or hybrid stability is expressed as the melting temperature or Tm, which is the temperature at which a probe dissociates from a target DNA. This melting temperature is used to define the required stringency conditions.

For target sequences that are related and substantially identical to the corresponding sequence of SEQ ID NO: 1 to SEQ ID NO: 4 (such as allelic variants and SNPs), rather than identical, it is useful to first establish the lowest temperature at which only homologous hybridization occurs with a particular concentration of salt (*e.g.*, SSC or SSPE). Then, assuming that 1% mismatching results in a 1°C decrease in the Tm, the temperature of the final wash in the hybridization reaction is reduced accordingly (for example, if sequences having > 95% identity with the probe are sought, the final wash

temperature is decreased by 5°C). In practice, the change in Tm can be between 0.5°C and 1.5°C per 1% mismatch.

Examples of inventive oligonucleotides of length X (in nucleotides), as indicated by polynucleotide positions with reference to, *e.g.*, SEQ ID NO:1, include those corresponding to sets (sense and antisense sets) of consecutively overlapping oligonucleotides of length X, where the oligonucleotides within each consecutively overlapping set (corresponding to a given X value) are defined as the finite set of Z oligonucleotides from nucleotide positions:

n to (n + (X-1));

where n=1, 2, 3,…(Y-(X-1));

where Y equals the length (nucleotides or base pairs) of SEQ ID NO:1 (VALUE TO REFLECT LENGTH OF SEQ ID NO:1);

where X equals the common length (in nucleotides) of each oligonucleotide in the set (*e.g.*, X=20 for a set of consecutively overlapping 20-mers); and

where the number (Z) of consecutively overlapping oligomers of length X for a given SEQ ID NO of length Y is equal to Y-(X-1). For example Z= VALUE TO REFLECT LENGTH OF SEQ ID NO:1 -19= VALUE TO REFLECT LENGTH OF SEQ ID NO:1 for either sense or antisense sets of SEQ ID NO:1, where X=20.

Preferably, the set is limited to those oligomers that comprise at least one CpG, TpG or CpA dinucleotide.

Examples of inventive 20-mer oligonucleotides include the following set of VALUE TO REFLECT LENGTH OF SEQ ID NO:1 oligomers (and the antisense set complementary thereto), indicated by polynucleotide positions with reference to SEQ ID NO:1 1-20, 2-21, 3-22, 4-23, 5-24, ……
Preferably, the set is limited to those oligomers that comprise at least one CpG, TpG or CpA dinucleotide.

The present invention encompasses, for *each* of SEQ ID NO: 1 to SEQ ID NO: 20 (sense and antisense), multiple consecutively overlapping sets of oligonucleotides or modified oligonucleotides of length X, where, *e.g.*, X= 9, 10, 17, 20, 22, 23, 25, 27, 30 or 35 nucleotides.

The oligonucleotides or oligomers according to the present invention constitute effective tools useful to ascertain

genetic and epigenetic parameters of the genomic sequence corresponding to SEQ ID NO: 1 to SEQ ID NO: 4 . Preferred sets of such oligonucleotides or modified oligonucleotides of length X are those consecutively overlapping sets of oligomers corresponding to SEQ ID NO: 1 to SEQ ID NO: 20 (and to the complements thereof). Preferably, said oligomers comprise at least one CpG, TpG or CpA dinucleotide.

Particularly preferred oligonucleotides or oligomers according to the present invention are those in which the cytosine of the CpG dinucleotide (or of the corresponding converted TpG or CpA dinculeotide) sequences is within the middle third of the oligonucleotide; that is, where the oligonucleotide is, for example, 13 bases in length, the CpG, TpG or CpA dinucleotide is positioned within the fifth to ninth nucleotide from the 5'-end.

The oligonucleotides of the invention can also be modified by chemically linking the oligonucleotide to one or more moieties or conjugates to enhance the activity, stability or detection of the oligonucleotide. Such moieties or conjugates include chromophores, fluorophors, lipids such as cholesterol, cholic acid, thioether, aliphatic chains, phospholipids, polyamines, polyethylene glycol (PEG), palmityl moieties, and others as disclosed in, for example, United States Patent Numbers 5,514,758, 5,565,552, 5,567,810, 5,574,142, 5,585,481, 5,587,371, 5,597,696 and 5,958,773. The probes may also exist in the form of a PNA (peptide nucleic acid) which has particularly preferred pairing properties. Thus, the oligonucleotide may include other appended groups such as peptides, and may include hybridization-triggered cleavage agents (Krol et al., *BioTechniques* 6:958-976, 1988) or intercalating agents (Zon, *Pharm. Res.* 5:539-549, 1988). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a chromophore, fluorophor, peptide, hybridization-triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The oligonucleotide may also comprise at least one art-recognized modified sugar and/or base moiety, or may comprise a modified backbone or non-natural internucleoside linkage.

The oligonucleotides or oligomers according to particular embodiments of the present invention are typically used in

'sets,' which contain at least one oligomer for analysis of each of the CpG dinucleotides of genomic sequence SEQ ID NO: 1 to SEQ ID NO: 4 and sequences complementary thereto, or to the corresponding CpG, TpG or CpA dinucleotide within a sequence of the pretreated nucleic acids according to SEQ ID NO: 5 to SEQ ID NO: 20 and sequences complementary thereto. However, it is anticipated that for economic or other factors it may be preferable to analyze a limited selection of the CpG dinucleotides within said sequences, and the content of the set of oligonucleotides is altered accordingly.

Therefore, in particular embodiments, the present invention provides a set of at least two (2) (oligonucleotides and/or PNA-oligomers) useful for detecting the cytosine methylation state in pretreated genomic DNA (SEQ ID NO: 5 to SEQ ID NO: 20), or in genomic DNA (SEQ ID NO: 1 to SEQ ID NO: 4 and sequences complementary thereto). These probes enable diagnosis, classification and/or therapy of genetic and epigenetic parameters of prostate cell proliferative disorders. The set of oligomers may also be used for detecting single nucleotide polymorphisms (SNPs) in pretreated genomic DNA (SEQ ID NO: 5 to SEQ ID NO: 20), or in genomic DNA (SEQ ID NO: 1 to SEQ ID NO: 4 and sequences complementary thereto).

In preferred embodiments, at least one, and more preferably all members of a set of oligonucleotides is bound to a solid phase.

In further embodiments, the present invention provides a set of at least two (2) oligonucleotides that are used as 'primer' oligonucleotides for amplifying DNA sequences of one of SEQ ID NO: 1 to SEQ ID NO: 20 and sequences complementary thereto, or segments thereof.

It is anticipated that the oligonucleotides may constitute all or part of an "array" or "DNA chip" (*i.e.*, an arrangement of different oligonucleotides and/or PNA-oligomers bound to a solid phase). Such an array of different oligonucleotide- and/or PNA-oligomer sequences can be characterized, for example, in that it is arranged on the solid phase in the form of a rectangular or hexagonal lattice. The solid-phase surface may be composed of silicon, glass, polystyrene, aluminum, steel, iron, copper, nickel, silver, or gold. Nitrocellulose as well as plastics such as nylon, which can exist in the form

of pellets or also as resin matrices, may also be used. An. overview of the Prior Art in oligomer array manufacturing can be gathered from a special edition of Nature Genetics (*Nature Genetics Supplement*, Volume 21, January 1999, and from the literature cited therein). Fluorescently labeled probes are often used for the scanning of immobilized DNA arrays. The simple attachment of Cy3 and Cy5 dyes to the 5'-OH of the specific probe are particularly suitable for fluorescence labels. The detection of the fluorescence of the hybridized probes may be carried out, for example, via a confocal microscope. Cy3 and Cy5 dyes, besides many others, are commercially available.

It is particularly preferred that the oligomers according to the invention are utilised for at least one of: detection of; detection and differentiation between or among subclasses of; diagnosis of; prognosis of; treatment of; monitoring of; and treatment and monitoring of prostate cell proliferative disorders. This is enabled by use of said sets for the detection or detection and differentiation of prostate cell proliferative disorders.

The present invention further provides a method for ascertaining genetic and/or epigenetic parameters of the genes GSTP1, HISTONE H4, PROSTAGLANDIN E2 RECEPTOR and ORPHAN NUCLEAR RECEPTOR NR5A2 and their regulatory regionsincluding genomic sequences according to SEQ ID NO: 1 to SEQ ID NO: 4 within a subject by analyzing cytosine methylation and single nucleotide polymorphisms. Said method comprising contacting a nucleic acid comprising one or more of the genes GSTP1, HISTONE H4, PROSTAGLANDIN E2 RECEPTOR and ORPHAN NUCLEAR RECEPTOR NR5A2 and their regulatory regions including genomic sequences according to SEQ ID NO: 1 to SEQ ID NO: 4 in a biological sample obtained from said subject with at least one reagent or a series of reagents, wherein said reagent or series of reagents, distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. Preferably, said method comprises the following steps: In the *first step*, a sample of the tissue to be analysed is obtained. The source may be any suitable source, such as cell lines, histological slides, biopsies, tissue embedded in paraffin,

bodily fluids, ejaculate, urine, blood and all possible combinations thereof.The DNA is then isolated from the sample. Extraction may be by means that are standard to one skilled in the art, including the use of commercially available kits, detergent lysates, sonification and vortexing with glass beads. Once the nucleic acids have been extracted, the genomic double stranded DNA is used in the analysis.

In the *second step* of the method, the genomic DNA sample is treated in such a manner that cytosine bases which are unmethylated at the 5'-position are converted to uracil, thymine, or another base which is dissimilar to cytosine in terms of hybridization behavior. This will be understood as 'pretreatment' herein.

The above described treatment of genomic DNA is preferably carried out with bisulfite (hydrogen sulfite, disulfite) and subsequent alkaline hydrolysis which results in a conversion of non-methylated cytosine nucleobases to uracil or to another base which is dissimilar to cytosine in terms of base pairing behavior.

In the *third step* of the method, fragments of the pretreated DNA are amplified, using sets of primer oligonucleotides according to the present invention, and an amplification enzyme. The amplification of several DNA segments can be carried out simultaneously in one and the same reaction vessel. Typically, the amplification is carried out using a polymerase chain reaction (PCR). The set of primer oligonucleotides includes at least two oligonucleotides whose sequences are each reverse complementary, identical, or hybridize under stringent or highly stringent conditions to an at least 16-base-pair long segment of the base sequences of one or more of SEQ ID NO: 5 to SEQ ID NO: 20 and sequences complementary thereto.

In an alternate embodiment of the method, the methylation status of preselected CpG positions within the nucleic acid sequences comprising one or more of SEQ ID NO: 1 to SEQ ID NO: 4 may be detected by use of methylation-specific primer oligonucleotides. This technique (MSP) has been described in United States Patent No. 6,265,171 to Herman. The use of methylation status specific primers for the amplification of bisulfite treated DNA allows the differentiation between

methylated and unmethylated nucleic acids. MSP primers pairs contain at least one primer which hybridizes to a bisulfite treated CpG dinucleotide. Therefore, the sequence of said primers comprises at least one CpG dinucleotide. MSP primers specific for non-methylated DNA contain a "T' at the 3' position of the C position in the CpG. Preferably, therefore, the base sequence of said primers is required to comprise a sequence having a length of at least 9 nucleotides which hybridizes to a pretreated nucleic acid sequence according to one of SEQ ID NO: 5 to SEQ ID NO: 20 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG dinucleotide.

A further preferred embodiment of the method comprises the use of *blocker* oligonucleotides. The use of such blocker oligonucleotides has been described by Yu et al., *BioTechniques* 23:714-720, 1997. Blocking probe oligonucleotides are hybridized to the bisulfite treated nucleic acid concurrently with the PCR primers. PCR amplification of the nucleic acid is terminated at the 5' position of the blocking probe, such that amplification of a nucleic acid is suppressed where the complementary sequence to the blocking probe is present. The probes may be designed to hybridize to the bisulfite treated nucleic acid in a methylation status specific manner. For example, for detection of methylated nucleic acids within a population of unmethylated nucleic acids, suppression of the amplification of nucleic acids which are unmethylated at the position in question would be carried out by the use of blocking probes comprising a 'CpA' or 'TpA' at the position in question, as opposed to a 'CpG' if the suppression of amplification of methylated nucleic acids is desired.

For PCR methods using blocker oligonucleotides, efficient disruption of polymerase-mediated amplification requires that blocker oligonucleotides not be elongated by the polymerase. Preferably, this is achieved through the use of blockers that are 3'-deoxyoligonucleotides, or oligonucleotides derivitized at the 3' position with other than a "free" hydroxyl group. For example, 3'-O-acetyl oligonucleotides are representative of a preferred class of blocker molecule.

Additionally, polymerase-mediated decomposition of the blocker oligonucleotides should be precluded. Preferably, such

preclusion comprises either use of a polymerase lacking 5'-3' exonuclease activity, or use of modified blocker oligonucleotides having, for example, thioate bridges at the 5'-terminii thereof that render the blocker molecule nuclease-resistant. Particular applications may not require such 5' modifications of the blocker. For example, if the blocker- and primer-binding sites overlap, thereby precluding binding of the primer (*e.g.*, with excess blocker), degradation of the blocker oligonucleotide will be substantially precluded. This is because the polymerase will not extend the primer toward, and through (in the 5'-3' direction) the blocker—a process that normally results in degradation of the hybridized blocker oligonucleotide.

A particularly preferred blocker/PCR embodiment, for purposes of the present invention and as implemented herein, comprises the use of peptide nucleic acid (PNA) oligomers as blocking oligonucleotides. Such PNA blocker oligomers are ideally suited, because they are neither decomposed nor extended by the polymerase.

Preferably, therefore, the base sequence of said *blocking oligonucleotides* is required to comprise a sequence having a length of at least 9 nucleotides which hybridizes to a pretreated nucleic acid sequence according to one of SEQ ID NO: 5 to SEQ ID NO: 20 and sequences complementary thereto, wherein the base sequence of said oligonucleotides comprises at least one CpG, TpG or CpA dinucleotide.

The fragments obtained by means of the amplification can carry a directly or indirectly detectable label. Preferred are labels in the form of fluorescence labels, radionuclides, or detachable molecule fragments having a typical mass which can be detected in a mass spectrometer. Where said labels are mass labels, it is preferred that the labeled amplificates have a single positive or negative net charge, allowing for better detectability in the mass spectrometer. The detection may be carried out and visualized by means of, *e.g.*, matrix assisted laser desorption/ionization mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI).

Matrix Assisted Laser Desorption/Ionization Mass Spectrometry (MALDI-TOF) is a very efficient development for

the analysis of biomolecules (Karas & Hillenkamp, *Anal Chem.*, 60:2299-301, 1988). An analyte is embedded in a light-absorbing matrix. The matrix is evaporated by a short laser pulse thus transporting the analyte molecule into the vapour phase in an unfragmented manner. The analyte is ionized by collisions with matrix molecules. An applied voltage accelerates the ions into a field-free flight tube. Due to their different masses, the ions are accelerated at different rates. Smaller ions reach the detector sooner than bigger ones. MALDI-TOF spectrometry is well suited to the analysis of peptides and proteins. The analysis of nucleic acids is somewhat more difficult (Gut & Beck, *Current Innovations and Future Trends*, 1:147-57, 1995). The sensitivity with respect to nucleic acid analysis is approximately 100-times less than for peptides, and decreases disproportionally with increasing fragment size. Moreover, for nucleic acids having a multiply negatively charged backbone, the ionization process via the matrix is considerably less efficient. In MALDI-TOF spectrometry, the selection of the matrix plays an eminently important role. For desorption of peptides, several very efficient matrixes have been found which produce a very fine crystallisation. There are now several responsive matrixes for DNA, however, the difference in sensitivity between peptides and nucleic acids has not been reduced. This difference in sensitivity can be reduced, however, by chemically modifying the DNA in such a manner that it becomes more similar to a peptide. For example, phosphorothioate nucleic acids, in which the usual phosphates of the backbone are substituted with thiophosphates, can be converted into a charge-neutral DNA using simple alkylation chemistry (Gut & Beck, *Nucleic Acids Res.* 23: 1367-73, 1995). The coupling of a charge tag to this modified DNA results in an increase in MALDI-TOF sensitivity to the same level as that found for peptides. A further advantage of charge tagging is the increased stability of the analysis against impurities, which makes the detection of unmodified substrates considerably more difficult.

In the *fourth step* of the method, the amplificates obtained during the third step of the method are analysed in order to ascertain the methylation status of the CpG dinucleotides prior to the treatment.

In embodiments where the amplificates were obtained by means of MSP amplification, the presence or absence of an amplificate is in itself indicative of the methylation state of the CpG positions covered by the primer, according to the base sequences of said primer.

Amplificates obtained by means of both standard and methylation specific PCR may be further analyzed by means of hybridization-based methods such as, but not limited to, array technology and probe based technologies as well as by means of techniques such as sequencing and template directed extension.

In one embodiment of the method, the amplificates synthesised in *step three* are subsequently hybridized to an array or a set of oligonucleotides and/or PNA probes. In this context, the hybridization takes place in the following manner: the set of probes used during the hybridization is preferably composed of at least 2 oligonucleotides or PNA-oligomers; in the process, the amplificates serve as probes which hybridize to oligonucleotides previously bonded to a solid phase; the non-hybridized fragments are subsequently removed; said oligonucleotides contain at least one base sequence having a length of at least 9 nucleotides which is reverse complementary or identical to a segment of the base sequences specified in the present Sequence Listing; and the segment comprises at least one CpG , TpG or CpA dinucleotide.

In a preferred embodiment, said dinucleotide is present in the central third of the oligomer. For example, wherein the oligomer comprises one CpG dinucleotide, said dinucleotide is preferably the fifth to ninth nucleotide from the 5'-end of a 13-mer. One oligonucleotide exists for the analysis of each CpG dinucleotide within the sequence according to SEQ ID NO: 1 to SEQ ID NO: 4 , and the equivalent positions within SEQ ID NO: 5 to SEQ ID NO: 20. Said oligonucleotides may also be present in the form of peptide nucleic acids. The non-hybridized amplificates are then removed.The hybridized amplificates are then detected. In this context, it is preferred that labels attached to the amplificates are identifiable at each position of the solid phase at which an oligonucleotide sequence is located.

In yet a further embodiment of the method, the genomic methylation status of the CpG positions may be ascertained by

means of oligonucleotide probes that are hybridised to the bisulfite treated DNA concurrently with the PCR amplification primers (wherein said primers may either be methylation specific or standard).

A particularly preferred embodiment of this method is the use of fluorescence-based Real Time Quantitative PCR (Heid et al., *Genome Res.* 6:986-994, 1996; *also see* United States Patent No. 6,331,393) employing a dual-labeled fluorescent oligonucleotide probe (TaqMan™ PCR, using an ABI Prism 7700 Sequence Detection System, Perkin Elmer Applied Biosystems, Foster City, California). The TaqMan™ PCR reaction employs the use of a nonextendible interrogating oligonucleotide, called a TaqMan™ probe, which, in preferred imbodiments, is designed to hybridize to a GpC-rich sequence located between the forward and reverse amplification primers. The TaqMan™ probe further comprises a fluorescent "reporter moiety" and a "quencher moiety" covalently bound to linker moieties (*e.g.*, phosphoramidites) attached to the nucleotides of the TaqMan™ oligonucleotide. For analysis of methylation within nucleic acids subsequent to bisulfite treatment, it is required that the probe be methylation specific, as described in United States Patent No. 6,331,393, (hereby incorporated by reference in its entirety) also known as the MethylLight™ assay. Variations on the TaqMan™ detection methodology that are also suitable for use with the described invention include the use of dual-probe technology (Lightcycler™) or fluorescent amplification primers (Sunrise™ technology). Both these techniques may be adapted in a manner suitable for use with bisulfite treated DNA, and moreover for methylation analysis within CpG dinucleotides.

A further suitable method for the use of probe oligonucleotides for the assessment of methylation by analysis of bisulfite treated nucleic acids In a further preferred embodiment of the method, the *fifth step* of the method comprises the use of template-directed oligonucleotide extension, such as MS-SNuPE as described by Gonzalgo & Jones, *Nucleic Acids Res.* 25:2529-2531, 1997.

In yet a further embodiment of the method, the *fifth step* of the method comprises sequencing and subsequent sequence analysis of the amplificate generated in the *third step* of the

method (Sanger F., et al., *Proc Natl Acad Sci USA* 74:5463-5467, 1977).

Best mode

In the most preferred embodiment of the method the nucleic acids according to SEQ ID NO: 1 to SEQ ID NO 4 are isolated and treated according to the first three steps of the method outlined above, namely:

a. obtaining, from a subject, a biological sample having subject genomic DNA;
b. extracting or otherwise isolating the genomic DNA;
c. treating the genomic DNA of b), or a fragment thereof, with one or more reagents to convert cytosine bases that are unmethylated in the 5-position thereof to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties;

and wherein the subsequent amplification of d) is carried out in a methylation specific manner, namely by use of methylation specific primers or *blocking oligonucleotides*, and further wherein the detection of the amplificates is carried out by means of a real-time detection probes, as described above.

Wherein the subsequent amplification of d) is carried out by means of methylation specific primers, as described above, said methylation specific primers comprise a sequence having a length of at least 9 nucleotides which hybridizes to a pretreated nucleic acid sequence according to one of SEQ ID NO: 5 to SEQ ID NO: 20 and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG dinucleotide. Step e) of the method, namely the detection of the specific amplificates indicative of the methylation status of one or more CpG positions according to SEQ ID NO: 1 to SEQ ID NO 4 is carried out by means of real-time detection methods as described above.

In an alternative most preferred embodiment of the method the subsequent amplification of d) is carried out in the presence of *blocking oligonucleotides*, as described above. Said *blocking oligonucleotides* comprising a sequence having a length of at least 9 nucleotides which hybridizes to a pretreated nucleic acid sequence according to one of SEQ ID NO: 5 to SEQ ID NO: 20

and sequences complementary thereto, wherein the base sequence of said oligomers comprises at least one CpG, TpG or CpA dinucleotide. Step e) of the method, namely the detection of the specific amplificates indicative of the methylation status of one or more CpG positions according to SEQ ID NO: 1 to SEQ ID NO 4 is carried out by means of real-time detection methods as described above.

14 14 14

Diagnostic and/or Prognostic Assays for prostate cell proliferative disorders

The present invention enables diagnosis of events which are disadvantageous to patients or individuals in which important genetic and/or epigenetic parameters within one or more of the genes GSTP1, HISTONE H4, PROSTAGLANDIN E2 RECEPTOR and ORPHAN NUCLEAR RECEPTOR NR5A2 and their regulatory regions including genomic sequences according to SEQ ID NO: 1 to SEQ ID NO: 4 may be used as markers. Said parameters obtained by means of the present invention may be compared to another set of genetic and/or epigenetic parameters, the differences serving as the basis for a diagnosis and/or prognosis of events which are disadvantageous to patients or individuals.

Specifically, the present invention provides for diagnostic and/or prognostic cancer assays based on measurement of differential methylation of one or more CpG dinucleotide sequences of the genes GSTP1, HISTONE H4, PROSTAGLANDIN E2 RECEPTOR and ORPHAN NUCLEAR RECEPTOR NR5A2 and their regulatory regions including genomic sequences according to SEQ ID NO: 1 to SEQ ID NO: 4 , or of subregions thereof that comprise such a CpG dinucleotide sequence. Typically, such assays involve obtaining a tissue sample from a test tissue, performing an assay to measure the methylation status of at least one of one or more CpG dinucleotide sequences of the genes GSTP1, HISTONE H4, PROSTAGLANDIN E2 RECEPTOR and ORPHAN NUCLEAR RECEPTOR NR5A2 and their regulatory regions including genomic sequences according to SEQ ID NO: 1 to SEQ ID NO: 4 derived from the tissue sample, relative to a control sample, or a known standard and making a diagnosis or prognosis based thereon.

In particular preferred embodiments, inventive oligomers are used to assess the CpG dinucleotide methylation status, such as those based on SEQ ID NO: 1 to SEQ ID NO: 20, or arrays thereof, as well as in kits based thereon and useful for the diagnosis and/or prognosis of prostate cell proliferative disorders.

Kits

Moreover, an additional aspect of the present invention is a kit comprising, for example: a bisulfite-containing reagent; a set of primer oligonucleotides containing at least two oligonucleotides whose sequences in each case correspond, are complementary, or hybridize under stringent or highly stringent conditions to a 16-base long segment of one or more of the genes GSTP1, HISTONE H4, PROSTAGLANDIN E2 RECEPTOR and ORPHAN NUCLEAR RECEPTOR NR5A2 and their regulatory regions including genomic and/or treated sequences according to SEQ ID NO: 1 to SEQ ID NO: 20; oligonucleotides and/or PNA-oligomers; as well as instructions for carrying out and evaluating the described method. In a further preferred embodiment, said kit may further comprise standard reagents for performing a CpG position-specific methylation analysis, wherein said analysis comprises one or more of the following techniques: MS-SNuPE, MSP, MethyLight ™, HeavyMethyl™ , COBRA, and nucleic acid sequencing. However, a kit along the lines of the present invention can also contain only part of the aforementioned components.

While the present invention has been described with specificity in accordance with certain of its preferred embodiments, the following example serves only to illustrate the invention and is not intended to limit the invention within the principles and scope of the broadest interpretations and equivalent configurations thereof.

EXAMPLES

The objective of the following study was to analyze the methylation status of prostate cancer markers in different body fluid samples in order to identify the preferred choice of body

fluid (urine or serum) for testing and the preferred marker, markers or combinations of markers. The study was run on matched serum and urine sediment samples from 80 patients with an average age of 65 and representative of a number of racial types (caucasian, african american etc..). In each case, genomic DNA was analyzed using the HeavyMethyl or MSP technique after bisulfite conversion.

Urine Sediment was prepared for analysis and bisulphite treated according to the following:

- 200 ul sediment samples were purified using the Magnapure DNA Isolation Kit 1 with a 100 ul elution volume.
- 5 ul HD6 PCR was carried out on the Magnapure Eluate , in order to determine DNA concentration
- 100 ul of the DNA solution was treated using a proprietary bisulfite treatment technique
- 10 ul C3 bisulfite specific quantitative PCR
- 5 ul Merck sulfite test

Serum was prepared for analysis and bisulphite treated according to the following:

- 1 mL serum samples were purified using the Magnapure DNA Large Volume Total nucleic acid with a 100 ul elution volume.
- 5 ul HD6 PCR on Magnapure Eluate - To determine DNA concentration
- 100 ul of the DNA solution was treated using a proprietary bisulfite treatment technique
- 10 ul C3 bisulfite specific quantitative PCR
- 5 ul Merck sulfite test

Single PCR runs were performed on 10 ul of bisulfite treated DNA per sample for each of the markers as described below.

Heavy Methyl Assay of the GSTP1 gene

In the following analysis the methylation status of the gene GSTP1 was analysed by means of methylation specific amplification using the primers according to Table 1 (below).

The sequence of interest is amplified by means of methylation specific primers and a blocker oligonucleotide in order to minimise the unspecific amplification of non methylated DNA. The amplificate is then detected by means of methylation specific Lightcycler probes.

Table 1: Oligonucleotides for MSP - Lightcycler analysis of GSTP1.

SEQ ID NO:	Sequence	Type
21	gggattatttttataaggtt	primer
22	ctctaaaccccatcccc	primer
23	cccatccccaaaaacacaaaccac	blocker
24	CGtCGtCGtAGTtTTCGtt-fluo	probe
25	red640-tAGTGAGTACGCGCGGtt-pho	probe

Reaction conditions:

PCR program

denat at 95°C

95°C 10min

50 cycles: ramp

denat at 95°C 10 sec (1°C/s)

annealing 56C°C30 sec (1°C/s) detection

extension 72°C 10 sec (1°C/s)

MSP analysis of the gene HISTONE H4.

In the following analysis the methylation status of the gene HISTONE H4 was analysed by means of methylation specific

amplification using the primers according to Table 2 (below).

The sequence of interest is amplified by means of methylation specific primers, the amplificate is then detected by means of methylation specific Taqman probes.

Table 2: Oligonucleotides for MSP - Taqman analysis of HISTONE H4.

SEQ ID NO :	Sequence	Type
26	accgaaaatacgcttcacg	primer
27	gcgttatcgtaaagtattgcgc	primer
28	/56-FAM/cgcgacgaacaaaacgccg/3BHQ_1/	probe

Reaction Conditions:

PCR program

denat at 95°C

95°C 10min

50 cycles: ramp

denat at 95°C 10 sec (20°C/s)

annealing 60C°C45 sec (20°C/s) detection

MSP analysis of the gene PROSTAGLANDIN E2 RECEPTOR.

In the following analysis the methylation status of the gene PROSTAGLANDIN E2 RECEPTOR was analysed by means of methylation specific amplification using the primers according to Table 3 (below).

The sequence of interest is amplified by means of methylation specific primers, the amplificate is then detected by means of methylation specific Taqman probes.

Table 3: Oligonucleotides for MSP - Taqman analysis of PROSTAGLANDIN E2 RECEPTOR

SEQ ID NO :	Sequence	Type
29	cgcgctactccgcataca	primer
30	gaggtaatcgaggcggtcg	primer
31	/56-FAM/cgccaattcatacgccgcacc/3BHQ_1/	probe

PCR program

denat at 95°C

95°C 10min

50 cycles: ramp

denat at 95°C 10 sec (20°C/s)

annealing 60C°C45 sec (20°C/s) detection

MSP analysis of the gene ORPHAN NUCLEAR RECEPTOR NR5A2.

In the following analysis the methylation status of the gene ORPHAN NUCLEAR RECEPTOR NR5A2 was analysed by means of methylation specific amplification using the primers according to Table 3 (below).

The sequence of interest is amplified by means of methylation specific primers, the amplificate is then detected by means of methylation specific Taqman probes.

Table 4: Oligonucleotides for MSP - Taqman analysis of ORPHAN NUCLEAR RECEPTOR NR5A2.

SEQ ID NO :	Sequence	Type
32	ttgtggttcgggaagagac	primer
33	tcccgaactcttcgatcg	primer
34	aactacgcgcaaacccgcga	probe

PCR program

denat at 95°C

95°C	10min	

50 cycles:

		ramp	
denat at 95°C	10 sec	(20°C/s)	
annealing 60C°C	45 sec	(20°C/s)	detection

Marker Analysis

Results were analyzed qualitatively by scoring amplification as +/- and quantitatively by determining the percentage of methylated DNA as a fraction of total DNA calculated using the C3 bisulfite specific PCR. To measure total methylated DNA, a 100% methylated standard (chemicon SSS1 treated DNA) standard curve was included in each assay.

Results

For each marker a Receiver Operating Characteristic curve (ROC curve) of the assay was determined. A ROC is a plot of the true positive rate against the false positive rate for the different possible cutpoints of a diagnostic test. It shows the tradeoff between sensitivity and specificity depending on the selected cutpoint (any increase in sensitivity will be accompanied by a decrease in specificity).The area under an ROC curve (AUC) is a measure for the accuracy of a diagnostic test (the larger the area the better, optimum is 1, a random test would have a ROC curve lying on the diagonal with an area of 0.5; for reference: J.P. Egan. Signal Detection Theory and ROC Analysis, Academic Press, New York, 1975).

AUC results:

Serum:

Marker: HevyMethyl GSTP1

AUC: 0.51

Marker: MSP HISTONE H4

AUC: 0.59

Marker: MSP PROSTAGLANDIN E2 RECEPTOR
AUC: 0.52
Marker: MSP ORPHAN NUCLEAR RECEPTOR NR5A2
AUC: 0.50

Urine:
Marker: HeavyMethyl GSTP1
AUC: 0.58
Marker: MSP HISTONE H4
AUC: 0.5
Marker: MSP PROSTAGLANDIN E2 RECEPTOR
AUC: 0.49
Marker: MSP ORPHAN NUCLEAR RECEPTOR NR5A2
AUC: 0.56

In order to provide an accurate detection of prostate cancer it is preferred that a combined analysis of multiple markers is carried out (i.e. a gene panel). For analysis of urine based samples the most preferred combination of markers is GSTP1 , PROSTAGLANDIN E2 RECEPTOR & ORPHAN NUCLEAR RECEPTOR NR5A2 with a sensitivity of 0.37 and a specificity of 0.72.
For analysis of serum based samples the most preferred combination of markers is GSTP1 , HISTONE H4 & ORPHAN NUCLEAR RECEPTOR NR5A2 with a sensitivity of 0.35 and a specificity of 0.75.

Table 5: Genes & Sequences according to the invention

Gene Name	Genbank Ref. Seq.	Genomic sequence SEQ ID NO:	Treated sequences (methylated) SEQ ID NO:	Treated sequences (unmethylated) SEQ ID NO:
GSTP1	NM_000852	1	5 & 6	13 & 14
HISTONE H4	NM_003495	2	7 & 8	15 & 16
PROSTAGLANDIN E2 RECEPTOR	NM_000958	3	9 & 10	17 & 18
ORPHAN NUCLEAR RECEPTOR NR5A2	NM_003822	4	11 & 12	19 & 20

We claim:

1. A method for detecting, or for detecting and distinguishing between or among prostate cell proliferative disorders in a subject with a sensitivity of greater than 30% and a specificity of greater than 65%, said method comprising analysing the methylation pattern of a target nucleic acid comprising one or a combination of sequences taken from the group consisting of SEQ ID Nos: 1-4 by contacting at least one of said target nucleic acids in a biological sample obtained from said subject with at least one reagent, or series of reagents that distinguishes between methylated and non-methylated CpG dinucleotides.

2. The method of claim 1, wherein prostate carcinoma is distinguished from at least one condition selected from the group consisting of prostate adenoma, normal prostate tissue, non-prostate tissues and non-prostate cell proliferative disorders.

3. A method according to claim 1, comprising:
-obtaining, from a subject, a biological sample having subject genomic DNA;
-contacting the genomic DNA, or a fragment thereof, with one reagent or a plurality of reagents for distinguishing between methylated and non methylated CpG dinucleotide sequences within at least one target sequence of the genomic DNA, or fragment thereof, wherein the target sequence comprises, or hybridizes under stringent conditions to, at least 16 contiguous nucleotides of a sequence taken from the group consisting of SEQ ID NO: 1 to SEQ ID NO 4 , said contiguous nucleotides comprising at least one CpG dinucleotide sequence; and
-determining, based at least in part on said distinguishing, the methylation state of at least one target CpG dinucleotide sequence, or an average, or a value reflecting an average methylation state of a plurality of target CpG dinucleotide sequences, whereby detecting, or detecting and distinguishing between or

among prostate cell proliferative disorders with a sensitivity of greater than 30% and a specificity of greater than 65% is, at least in part, afforded.

4. The method of claim 3, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises converting unmethylated cytosine bases within the target sequence to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties.

5. The method of claim 3, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence(s) comprises methylation state-dependent conversion or non-conversion of at least one CpG dinucleotide sequence to the corresponding converted or non-converted dinucleotide sequence within a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and contiguous regions thereof corresponding to the target sequence.

6. The method of claim 3, wherein the biological sample is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.

7. The method of claim 3, wherein distinguishing between methylated and non methylated CpG dinucleotide sequences within the target sequence comprises use of at least one nucleic acid molecule or peptide nucleic acid (PNA) molecule comprising, in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof.

8. The method of claim 7, wherein the contiguous sequence comprises at least one CpG, TpG or CpA dinucleotide sequence.

9. The method of claim 7, comprising use of at least two such nucleic acid molecules, or peptide nucleic acid (PNA) molecules.

10. The method of claim 7, comprising use of at least two such nucleic acid molecules, or peptide nucleic acid (PNA) molecules as primer oligonucleotides for the amplification of a sequences selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, sequences complementary thereto, and regions thereof that comprise, or hybridize under stringent conditions to the primers.

11. The method of claim 9, comprising use of at least four such nucleic acid molecules, or peptide nucleic acid (PNA) molecules.

12. A method for detecting, or detecting and distinguishing between or among prostate cell proliferative disorders in a subject, comprising:

a. obtaining, from a subject, a biological sample having subject genomic DNA;

b. extracting or otherwise isolating the genomic DNA;

c. treating the genomic DNA of b), or a fragment thereof, with one or more reagents to convert cytosine bases that are unmethylated in the 5-position thereof to uracil or to another base that is detectably dissimilar to cytosine in terms of hybridization properties;

d. contacting the treated genomic DNA, or the treated fragment thereof, with an amplification enzyme and at least two primers comprising, in each case a contiguous sequence of at least 9 nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof, wherein the treated genomic DNA or the fragment thereof is either amplified to produce at least one amplificate, or is not amplified; and

e) determining, based on a presence or absence of, or on a property of said amplificate, the methylation state of at least one CpG dinucleotide of a sequence selected from the group consisting SEQ ID NO: 1 to SEQ ID NO 4 , or an average, or a value reflecting an average methylation state of a plurality of CpG dinucleotides of a sequence selected from the groups consisting of SEQ ID NO: 1 to SEQ ID NO 4 , whereby at least one of detecting, or detecting and distinguishing between prostate cell proliferative disorders with a sensitivity of greater than 30% and a specificity of greater than 65% is at least in part, afforded.

13. The method of claim 12, wherein treating the genomic DNA, or the fragment thereof in c), comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof.

14. The method of claim 12, wherein contacting or amplifying in d) comprises use of at least one method selected from the group consisting of: use of a heat-resistant DNA polymerase as the amplification enzyme; use of a polymerase lacking 5'-3' exonuclease activity; use of a polymerase chain reaction (PCR); generation of a amplificate nucleic acid molecule carrying a detectable labels; and combinations thereof.

15. The method of claim 14, wherein the detectable amplificate label is selected from the label group consisting of: fluorescent labels; radionuclides or radiolabels; amplificate mass labels detectable in a mass spectrometer; detachable amplificate fragment mass labels detectable in a mass spectrometer; amplificate, and detachable amplificate fragment mass labels having a single-positive or single-negative net charge detectable in a mass spectrometer; and combinations thereof.

16. The method of claim 12, wherein the biological sample obtained from the subject is selected from the group consisting of cell lines, histological slides, biopsies, paraffin-embedded tissue, bodily fluids, ejaculate, urine, blood, and combinations thereof.

17. The method of claim 12, wherein prostate carcinoma is distinguished from at least one condition selected form the group consisting of prostate adenoma, inflammatory prostate tissue, prostate adenomas with grade 2 dysplasia less than 1 cm, prostate adenomas with grade 3 dysplasia equal to or greater than 1 cm in size, normal prostate tissues, non-prostate normal tissue, body fluids, and non-prostate cancer tissue.

18. The method of claim 12, further comprising in step d) the use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized.

19. The method of claim 18, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case modified at the 5'-end thereof to preclude degradation by an enzyme having 5'-3' exonuclease activity.

20. The method of claim 18, wherein said nucleic acid molecule or peptide nucleic acid molecule is in each case lacking a 3' hydroxyl group.

21. The method of claim 18, wherein the amplification enzyme is a polymerase lacking 5'-3' exonuclease activity.

22. The method of claim 12, wherein determining in e) comprises hybridization of at least one nucleic acid molecule or peptide nucleic acid molecule in each case comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO: 20, and complements thereof.

23. The method of claim 22, wherein at least one such hybridizing nucleic acid molecule or peptide nucleic acid molecule is bound to a solid phase.

24. The method of claim 22, wherein a plurality of such hybridizing nucleic acid molecules or peptide nucleic acid molecules are bound to a solid phase in the form of a nucleic acid or peptide nucleic acid array selected from the array group consisting of linear or substantially so, hexagonal or substantially so, rectangular or substantially so, and combinations thereof.

25. The method of claim 22, further comprising extending at least one such hybridized nucleic acid molecule by at least one nucleotide base.

26. The method of claim 12, wherein determining in e), comprises sequencing of the amplificate.

27. The method of claim 12, wherein contacting or amplifying in d), comprises use of methylation-specific primers.

28. The method of claim 12 comprising in d) using primer oligonucleotides comprising one or more CpG; TpG or CpA dinucleotides; and further comprising in e) the use of at least one method selected from the group consisting of: hybridizing in at least one nucleic acid molecule or peptide nucleid acid molecule comprising a contiguous sequence at least 9 nucleotides in length that

is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof; hybridizing at least one nucleic acid molecule that is bound to a solid phase and comprises a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing in e) of the amplificate.

29. The method of claim 12 comprising in d) use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized; and further comprising in e) the use of at least one method selected from the group consisting of: hybridizing in at least one nucleic acid molecule or peptide nucleid acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof; hybridizing at least one nucleic acid molecule that is bound to a solid phase and comprises a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under

moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof; hybridizing at least one nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof, and extending at least one such hybridized nucleic acid molecule by at least one nucleotide base; and sequencing in e) of the amplificate.

30. The method of claim 12, comprising in d) amplification by primer oligonucleotides comprising one or more CpG; TpG or CpA dinucleotides and further comprising in e) hybridizing at least one detectably labeled nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20.

31. The method of claim 12, comprising in d) the use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and complements thereof, wherein said nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of the nucleic acid to which it is hybridized, and further comprising in e) hybridizing at least one detectably labeled nucleic acid molecule comprising a contiguous sequence at least 9 nucleotides in length that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20.

32. 14 14 14 A treated nucleic acid derived from genomic SEQ ID NO: 1 to SEQ ID NO 4 , wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization.

33. A nucleic acid, comprising at least 16 contiguous nucleotides of a treated genomic DNA sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20, and sequences complementary thereto, wherein the treatment is suitable to convert at least one unmethylated cytosine base of the genomic DNA sequence to uracil or another base that is detectably dissimilar to cytosine in terms of hybridization.

34. The nucleic acid of claims 32 and 33 wherein the contiguous base sequence comprises at least one CpG, TpG or CpA dinucleotide sequence.

35. The nucleic acid of claims 32 and 33 wherein the treatment comprises use of a reagent selected from the group consisting of bisulfite, hydrogen sulfite, disulfite, and combinations thereof .

36. An oligomer, comprising a sequence of at least 9 contiguous nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a treated genomic DNA sequence selected from the group consisting of SEQ ID NO: 5 to SEQ ID NO 20.

37. The oligomer of Claim 36, comprising at least one CpG , CpA or TpG dinucleotide sequence.

38. An oligomer of claim 37, having a sequence selected from the group consisting of SEQ ID NO: &[IDOLIGOFIRST] to SEQ ID NO &[IDOLIGOLAST].

39. A set of oligomers, comprising at least two oligonucleotides according, in each case, to any one of Claims 37 or 38.

40. Use of a set of oligomers according, in each case, to any one of Claims 36 through 39, as probes for determining at least one of a cytosine methylation state, or a single nucleotide polymorphism (SNP) of a sequence selected from the group consisting of SEQ ID NO: 1 to 4 and sequences complementary thereto.

41.

42. A kit useful for detecting, or for detecting distinguishing between or among prostate cell proliferative disorders of a subject, comprising:

-at least one of a bisulfite reagent, or a methylation-sensitive restriction enzyme; and

-at least one nucleic acid molecule or peptide nucleic acid molecule comprising, in each case a contiguous sequence at least 9 nucleotides that is complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID 5 to SEQ ID NO 20, and complements thereof

43. The kit of claim 42, further comprising standard reagents for performing a methylation assay selected from the group consisting of MS-SNuPE, MSP, MethyLight, HeavyMethyl, COBRA, nucleic acid sequencing, and combinations thereof.

44. The method of any one of claims 1, 12 or 3 comprising use of the kit according to claim 53.

45. Use of a nucleic acid according to claims 32 through 35, an oligomer according to any one of claims 36 through 38, a set of oligonucleotides according to claim 39 and a kit according to claims 43 and 44 for the detection of,

detection and differentiation between or among subclasses of prostate cell proliferative disorders.

Abstract

The invention provides methods, nucleic acids and kits for detecting, or for detecting and distinguishing between or among prostate cell proliferative disorders. The invention discloses genomic sequences the methylation patterns of which have utility for the improved detection of and differentiation between said class of disorders, thereby enabling the improved diagnosis and treatment of patients.

<110> Epigenomics AG

<120> METHODS AND NUCLEIC ACIDS FOR THE ANALYSIS OF CpG DINUCLEOTIDE METHYLATION STATUS ASSOCIATED WITH THE DEVELOPMENT OF PROSTATE CANCER.

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<212> DNA
<213> Homo Sapiens

<400> 1

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<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 7

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<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2251
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 9

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<211> 2251
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2586
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

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<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 15

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<211> 2501
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

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<211> 2251
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 17

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gtgttatttg tgtgtatagt tttatatttg aatgttgttt ttttgtagat gagattggtg 180
ggtattgtaa agttgggatt tgtttttgaa ggaaaaaaaa tagtgagtaa gaaatttagt 240

attatttttt attgatttat tttgttgtat tttttgtttt ttaagttttt gaaagttggt 300
aattttgatt ttggtgttta aaaattgata gttattgaga ttggttttga gaagttgaag 360
atttggtagt ttttagattg agtaggataa ggtgaaagta ggttggaggt gggtttagga 420
tatttgaggg ttgattttgg gggtttgtga ggttgttatt gttgttgttg ttataggtga 480
gatggtgttg ggttgatgtt ggggttaatg ggtagagaat gtagggatgt ggtttttgtt 540
gaagagagtt aagaagggaa gagtgtgttt tttaaattgt ttttgtaatt tgtttttagt 600
gagtatttta ttgatttaga atttattgag aatagtatta gtgagttatt tttttttga 660
gatgggtttt atttattttg gtaatggagt gagttggatt gtggggagga agaggaatgg 720
gaaaattagt ttataaatat taatgttagt aagagtgtgt tgttggtagg atgtattgtg 780
agtttggaga ttttggtggt tgtagttggt aagtggttat aatttagaaa gtaggattga 840
gttgtttttt ttgttttatt agtgtattgt tttttgggtg tgggtttaat attttataag 900
tggtaatttt tgtttatggt agttttgttt tttttttatt atttttagat ttagttttgt 960
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gagtgattgg ggttggggtt ttatttggtt tttttttgt atttattttt tgtgtttatt 1920
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ttgggatttt tatattgttt tttagagtag gtttaatttt ttttgaagtt ttaattttaa 2040
tgagatttag taggtgtttt gtttttatat tttttagttt atgtttttgg aagtttgggt 2100
ttttttttt attgagatag tttttatttt ttgttgtttg atattggttg agttttttaa 2160
gaaaattttt tgttttttt gttagatgtg gaggggagtt tgttgtagtg tgatttagtt 2220
tatttttttg tattgtgaat tgtgaattgt a 2251

<210> 18
<211> 2251
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 18

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aggggtaagg gttgttttgg tggagaaaga aatttaggtt tttgggaata taaattgggg 180
gatgtagggg taaagtattt gttaaatttt gttagggttg ggattttaaa gagggttggg 240
tttgttttga gaaatagtgt gggaatttta gttttgattt aaaggtgata tgtttattgt 300
taaggattta gagggaaagt agggagtggg gaatggatgt gggaggtgga tgtgagaaaa 360
aggttgagta gggttttagt tttggttatt tattatgagt gggatggagt agatgagtat 420
tattagggag gtggtaatga gtaagatgat tatttggatt ttggtgtttg tgatgtggtg 480
gaagttttgg tggtgttgaa agttgttgag gtgtggtaag gttggggagg tagtggggtg 540
gttttgggag gtaattgagg tggttgtggt tgtgtggtgt tgtttggtgt ttagtgaggt 600
gtggtgtatg aattggtggt gtatgtggag tagtgtgttg tatataagta tgttgtagag 660
gatggtggtg agaatgagga aggagttgaa gtttgtgtat atgtaggagt aggtggtgtg 720
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aatgatatat tgataagata aggggagtaa tttgatttta ttttttggat tgtagttatt 1440
tattaattgt ggttattaaa atttttaggt ttgtgatatg ttttgttaat agtatatttt 1500
tgttgatatt aatatttata aattgatttt tttatttttt ttttttttta taatttaatt 1560

tattttattg ttaagatgaa taagatttat tttaagggaa aagtagtttg ttagtgttat 1620
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tttttggtta tttgggggtg gtttggggtt t 2251

<210> 19
<211> 2586
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 19

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agtaatgttt aattggttgt ttttaattaa ggaaagagag gtttttagtt ttatggtaat 180
ttaagtaggg tagttttagg ttaaaggtat tttagaataa taagattatt ttaagaaatg 240
gaatgtttta ttggatattt gaataggttt tttgttattg gaattggtgt gtattgtatt 300
ttaattagta tttttgtgtg gagggaggtg atttagttta ggaaagttaa ttatagaaag 360
aggtgatttt tgaaaggatt gttttagtgt tattagaata tatgtgatta tattaaaagt 420
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agggaataag ttattttaat tttatttttt gtatgtgtag tgttgagtga gttgggggtg 540
ggaggatagt ggtttgttta ttgtttttt ttaaaatttg agatttgaaa atatggaggt 600
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tgatttttt gatggttttt tttgattgaa gagtttggga attaaagaga aaaaaaataa 2520
ttttatttt aaaagaataa gttattattg tggtgatatt gtggtggagg attttggtga 2580
tggggt 2586

<210> 20
<211> 2586
<212> DNA

<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 20

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ataaagttat ttttttttt tttggttttt gagttttttg gttggaaagg gttgttaggg 120
gggttatttg tagtattttg tggttaagga ttgtgtgtag atttgtggag ttgatgtgtt 180
ttttttgggg ttatagagtt ttaggatggt ttatagggga gtgagttagt tagagtttgg 240
gaatattttg agaaaagagg ttttagagaa ggtaggagtt tgtttttgtg aaatattaat 300
aaagggatgt taggtgaggt ttttttagtg gtgttagttt gaattttagt tttaagagat 360
ttttattagg gttttaggaa tttgggggtt tgggaagggt tgagggttta gaaatttttt 420
tatagttttt agatgttgat agtttttttа ataattgtga tgatagtttt gaggtatgtt 480
ttaggaataa ggtgaaaagt gtatttttt aattgtgatt ttttttattt ttttttttt 540
taataaagta aattttaatt ttatattaaa ggggtataga taggtaattg tttttagagg 600
gattttgtgt ttattttggg gatttgatat tgaagaaaga ttgaggtatg aggtagagat 660
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tgtggg 2586

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 21

gggattattt ttataaggtt 20

<210> 22
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 22

ctctaaaccc catcccc 17

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 23

cccatcccca aaaacacaaa ccac 24

<210> 24
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 24

cgtcgtcgta gttttcgtt 19

<210> 25
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 25

tagtgagtac gcgcggtt 18

<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 26

accgaaaata cgcttcacg 19

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 27

gcgttatcgt aaagtattgc gc 22

<210> 28
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> chemically treated genomic DNA (Homo sapiens)

<400> 28

cgcgacgaac aaaacgccg 19

<210> 29
<211> 18
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<400> 29

cgcgctactc cgcataca 18

<210> 30
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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<400> 30

gaggtaatcg aggcggtcg 19

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 31

cgccaattca tacgccgcac c 21

<210> 32
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 32

ttgtggttcg ggaagagac 19

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 33

tcccgaactc ttcgatcg 18

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 34

aactacgcgc aaacccgcga 20

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COS													
direct													
aMedes	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AmpliTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AmpliTech_PuMaTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AssayDesign	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
autoimmune	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BaToPe	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Beutha_Bia_Replacing_Techs	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Beutha_Bia_Replacing_Techs_Device	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BetaW	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
bOCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
cell_drug_tech_feed	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Chiptop	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
compr marker mach_m ms	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
comprehensive marker machine	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
CRC_PM	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Device	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
DMH	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
dummy	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Endometriosis	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
EpiLMD	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
episcope	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
EU_breast	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
FuMaDaTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
KEP	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ILD	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
internal POs_before_feed	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
LOI_CRC	-8.063,75	-11.255,70	-8.178,70	-3.701,00	-1.198,00	-1.198,00	-1.198,00	-1.198,00	-8.148,00	-1.198,00	-1.198,00	-1.198,00	-43.111,14
marker machine improvement (FuMaTech)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
MeST_Bene	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
MeST_validation	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
methyl-ally	0,00	-43.841,00	-19.181,00	-23.757,00	-13.101,00	-13.318,00	-8.884,00	-10.418,00	-8.390,00	0,00	0,00	0,00	-144.708,00
miRNA	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Mlaclerosis	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
NHL_Screen	-8.649,88	-37.809,02	-52.508,38	-53.169,42	-38.334,80	-41.782,92	-19.877,51	-33.747,51	-119.883,08	-37.376,08	-40.723,80	-41.331,80	-482.374,06
paracra_tech_feed	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
pOs_new_drug	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Proteomics	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
PT_plattform_(alpha assay)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Qia_pool	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_BCS	-106.381,00	-78.633,00	-84.831,00	-84.131,00	-84.451,00	-85.469,00	-63.107,00	-63.107,00	-63.107,00	-44.817,00	-43.881,00	-43.831,00	-887.837,00
R_Bladder_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_CS	-91.605,67	-85.134,36	-87.112,81	-61.803,37	-23.587,00	-37.250,81	-3.083,00	-1.047,00	-58.327,78	0,00	0,00	-40.920,76	-435.401,[illegible]
R_overhead_project_budget_A0	-7.731,38	-7.731,38	-8.251,38	-7.731,38	-7.731,38	-11.531,38	-7.751,38	-7.751,38	-8.051,38	-7.751,38	-7.731,38	-7.731,38	-100.418,[illegible]
R_Project_Managementdoc	-18.819,00	-14.819,00	-19.419,00	-15.419,00	-19.419,00	-14.819,00	-19.778,43	-14.819,00	-14.819,00	-18.419,00	-19.624,63	-18.819,00	-209.627,06
R_Prostate_Cancer_MCT	-60.008,62	-63.906,62	-53.034,45	-110.818,00	-40.797,00	-23.373,00	-24.263,00	-24.291,63	-79.361,31	-61.137,62	-35.473,02	-35.473,02	-680.302,87
R_Prostate_CS	-104.374,07	-101.334,07	-111.938,07	-103.808,47	-103.784,47	-62.624,07	-43.836,13	-30.851,00	-8.336,00	0,00	0,00	0,00	-647.808,[illegible]
R_YAM	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ResearchAssays	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ReServ	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SampleDB	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SampleTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Sensitive_Detection	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Seqimp	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
tenascin_marker	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
VPA sep & cell lines	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
xenograft	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
allocation rest operative OC (not IT)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Total Projects (direct)	-416.801,88	-464.129,84	-370.838,88	-466.320,83	-270.711,76	-530.313,18	-181.536,77	-168.123,83	-333.333,71	-191.488,08	-180.763,83	-168.803,06	-3.430.108,70
Total Projects (allocation)	-71.818,64	-83.177,38	-76.663,77	-64.488,27	-74.204,71	-66.808,33	-63.184,86	-85.769,79	-70.766,77	-161.628,41	-104.418,80	-130.800,33	-1.041.830,40
Total Projects	-488.618,41	-544.306,40	-447.905,85	-510.830,80	-344.916,47	-648.320,80	-274.721,11	-254.828,50	-405.120,43	-353.118,47	-284.376,80	-298.803,38	-4.471.740,10
gross margin	180.538,07	-186.918,47	-87.316,70	65.008,88	-7.480,88	25.786,81	316.381,84	147.409,36	3.611.766,18	2.904.888,17	280.387,80	300.524,84	7.532.848,72
R&D													
direct													
aMedes	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AmpliTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AmpliTech_PuMaTech	-11.894,32	-13.177,74	-11.182,80	-11.779,25	-8.181,23	-8.181,23	-4.318,84	-4.028,37	-4.028,37	-3.876,88	0,00	0,00	-74.140,00
AssayDesign	-4.448,50	-4.230,00	-8.198,00	-9.508,00	-7.848,00	-11.843,83	-10.581,00	-10.480,00	-8.341,00	-6.131,00	-7.800,00	-6.636,11	-93.023,43
autoimmune	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BaToPe	-13.788,50	-13.338,50	-27.763,50	-15.843,50	-15.825,50	-35.322,50	-8.838,50	-8.480,50	-8.624,50	-8.815,50	-8.884,50	-8.884,50	-158.064,40
Beutha_Bia_Replacing_Techs	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Beutha_Bia_Replacing_Techs_Device	-7.060,00	-8.018,00	-10.518,13	-8.017,00	-8.187,00	-6.197,00	-3.543,58	-4.178,83	-3.140,00	-3.873,58	-4.733,77	-3.630,00	-64.411,67
BetaW	-4.354,00	-8.228,00	-3.725,00	-3.229,00	-4.254,00	-8.823,00	-3.725,00	-3.829,00	-2.758,00	-60,00	-60,00	-60,00	-47.763,00
bOCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
cell_drug_tech_feed	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Chiptop	-13.843,80	-15.464,43	-7.208,15	-1.898,18	-472,00	-12.474,10	-8.953,00	-4.177,16	-1.034,77	0,00	0,00	0,00	-64.814,81
compr marker mach_m ms	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
comprehensive marker machine	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
CRC_PM	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Device	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
DMH	-8.318,67	-9.763,67	-9.982,67	-11.711,67	-13.583,67	-12.598,67	-20.768,17	-17.008,67	-21.857,17	-21.844,67	-20.595,67	-14.871,17	-182.444,44
dummy	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Endometriosis	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
EpiLMD	-10.872,00	-8.760,00	-8.808,00	-8.308,00	-10.466,00	-8.783,00	-6.144,00	-8.787,00	-8.787,00	-8.598,00	-8.733,00	-6.478,00	-83.171,00
episcope	-8.007,00	-8.007,00	-8.007,00	-1.324,72	-1.324,72	-1.019,81	-8.029,88	-8.094,37	-8.094,37	-548,80	-383,78	-383,78	-81.808,42
EU_breast	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
FuMaDaTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
KEP	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ILD	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
internal POs_before_feed	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
LOI_CRC	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
marker machine improvement (FuMaTech)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
MeST_Bene	-15.874,67	-8.008,67	-1.370,00	0,00	0,00	-8.878,67	-8.608,67	-1.370,00	0,00	0,00	-8.608,67	-1.370,00	-80.681,35
MeST_validation	-10.787,37	-3.862,11	-8.358,78	-6.434,28	-7.325,88	-8.349,46	-8.677,84	-8.839,63	-8.829,63	-6.326,78	-6.326,78	-6.326,78	-77.476,71
methyl-ally	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
miRNA	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Mlaclerosis	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
NHL_Screen	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
paracra_tech_feed	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
pOs_new_drug	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Proteomics	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
PT_plattform_(alpha assay)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Qia_pool	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_BCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Bladder_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_overhead_project_budget_A0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Project_Managementdoc	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Prostate_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Prostate_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_YAM	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ResearchAssays	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ReServ	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SampleDB	-13.000,00	-13.688,00	-12.007,84	-10.843,00	-8.034,00	-8.171,30	-7.430,00	-7.117,00	-8.331,55	-8.311,44	-8.729,00	-8.915,00	-118.869,71
SampleTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Sensitive_Detection	-8.860,88	-9.380,83	-8.380,88	-7.508,89	-8.378,08	-67.008,18	-33.377,78	-32.448,32	-33.853,88	-34.843,32	-33.554,74	-38.533,74	-337.353,88
Seqimp	0,00	0,00	0,00	0,00	0,00	0,00	-8.201,00	-11.807,00	-28.125,00	-18.413,00	-7.848,00	0,00	-74.768,00
tenascin_marker	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
VPA sep & cell lines	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
xenograft	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
allocation rest operative OC (not IT)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Total Projects (direct)	-123.391,42	-118.815,70	-123.820,77	-93.887,18	-88.877,20	-103.203,00	-123.847,71	-129.123,87	-130.427,81	-113.723,76	-96.123,81	-76.764,78	-1.368.806,18
Total Projects (allocation)	-57.338,87	-54.905,88	-56.315,68	-42.146,88	-43.393,13	-47.823,41	-60.340,60	-66.363,08	-61.837,37	-70.843,21	-70.823,80	-94.870,48	-723.101,87
Total Projects	-180.730,30	-170.721,86	-180.136,48	-136.133,06	-136.270,32	-187.823,43	-183.823,38	-194.488,80	-193.323,18	-184.573,88	-168.958,60	-170.643,32	-2.087.608,43
Total OC	-43.772,33	-83.818,85	-86.828,12	-51.378,43	-57.228,34	-63.038,08	-43.843,30	-84.823,76	-71.478,18	-63.843,88	-68.439,70	-63.648,32	-681.760,82
BizDev													
Total	-53.353,74	-48.031,78	-43.391,71	-53.840,52	-54.403,62	-52.118,62	-53.533,81	-53.371,82	-41.394,32	-53.346,88	-51.184,83	-53.414,65	-611.833,81
Admin													
Total	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
profit/ loss	-63.823,88	-417.313,76	-408.848,88	-153.760,03	-435.808,87	-237.063,63	60.707,44	-130.808,38	3.318.572,61	2.494.394,88	21.808,67	18.786,04	4.387.788,13

PT	Pharma Tech Budget 2004												
	Jan. 04	Feb. 04	Mrz. 04	Apr. 04	Mai. 04	Jun. 04	Jul. 04	Aug. 04	Sep. 04	Okt. 04	Nov. 04	Dez. 04	Total 2004
REV	[illegible]	[illegible]	[illegible]	177.888,89	157.488,88	[illegible]	130.166,67	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
COGS													
direkt													
aMarker	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AmplTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AmplTech_PulsTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AssayDesign	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
autoImaging	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BioTyPe	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Bleeding_Bio_Replacing_Techn	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Bleeding_Bio_Replacing_Techn_Device	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BioLW	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BOCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
cell_drug_tech_food	0,00	0,00	0,00	-8.432,10	-31.251,10	-7.847,00	-31.464,00	-23.100,00	-7.540,00	0,00	0,00	0,00	[illegible]
Chipling	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
compr marker mech_as ma	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
comprehensive marker matching	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
CRC_PM	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Device	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
DMH	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
dummy	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Endometriosis	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
EpiLMG	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
episcape	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
EU_breast	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
PulsDxTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
HEP	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ILD	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
internal POs_before_food	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
LDI_CRC	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
marker matching improvement (PulsTech)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
MeGT_Bern	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
MeGT_validation	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
methylB-ally	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
mRNA	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Mastercells	0,00	0,00	-18.729,70	-1.843,00	-8.300,10	0,00	0,00	0,00	-33.712,00	-13.103,40	-8.804,00	0,00	[illegible]
NHL_Screen	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
paracrine_tech_food	-7.725,00	-13.452,00	-5.787,00	-8.308,00	-62.123,00	-7.311,00	0,00	0,00	0,00	0,00	0,00	0,00	[illegible]
POs_new_drug	0,00	0,00	0,00	0,00	0,00	0,00	-30.334,70	-8.342,10	-12.378,20	-23.916,00	-11.232,00	-13.316,00	[illegible]
Preselampels	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
PT_platform (alpha assay)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Ola_deal	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_BCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Bladder_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_overhead_project_budget_AG	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Project_Managementshc	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Prostate_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Prostate_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_TAM	-42.805,00	-44.443,00	-30.913,00	-28.294,00	-32.504,00	-21.132,00	-11.743,00	-8.853,00	-8.876,00	0,00	0,00	0,00	[illegible]
ResearchAssays	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ReServ	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SampleDB	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SampleTech	0,00	1,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Sensitive_Detection	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SeqInp	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
targeted_marker	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
VPA test & cell lines	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
xenograft	-21.054,20	-7.876,00	-11.061,20	-23.075,00	-14.113,20	-7.283,00	-8.461,00	0,00	0,00	0,00	0,00	0,00	[illegible]
allocation rest operative OC (not IT)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Total Projects (direct)	-91.763,[illegible]	-67.813,[illegible]	-67.303,[illegible]	-78.881,19	-138.831,4[illegible]	-43.499,[illegible]	-88.914,7[illegible]	-64.306,1[illegible]	-60.808,30	-43.919,[illegible]	-17.198,[illegible]	-13.316,00	-706.11[illegible]
Total Projects (allocation)	-18.742,4[illegible]	-13.040,87	-11.633,18	146,[illegible]	-3.767,[illegible]	-30.183,33	-15.183,[illegible]	-14.398,47	-4.366,47	-15.646,[illegible]	-60.607,[illegible]	[illegible]	-178.[illegible]
Total Projects	-103.488,0[illegible]	-86.863,07	-[illegible]	-78.830,77	-138.298,42	-[illegible]	-76.176,76	-82.488,57	-64.776,87	-[illegible]	-47.808,[illegible]	-[illegible]	-[illegible]
gross margin	102.829,81	108.888,3[illegible]	88.436,30	197.878,0[illegible]	62.301,87	34.681,4[illegible]	111.[illegible]	128.537,7[illegible]	62.447,[illegible]	73.171,67	[illegible]	-3.173,18	[illegible]
R&D													
direkt													
aMarker	-3.304,00	-8.708,00	-17.528,18	-20.074,83	-14.434,22	-15.734,[illegible]	-14.434,32	-15.184,47	-33.437,54	-19.830,11	-19.830,11	-18.058,6[illegible]	[illegible]
AmplTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AmplTech_PulsTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AssayDesign	-606,00	-1.211,00	-909,00	-1.212,00	-909,00	-2.077,10	-2.003,00	-1.429,00	-1.429,00	-1.837,00	-1.212,00	-1.863,37	-17.[illegible],47
autoImaging	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BioTyPe	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Bleeding_Bio_Replacing_Techn	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Bleeding_Bio_Replacing_Techn_Device	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BioLW	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BOCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
cell_drug_tech_food	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Chipling	-9.029,[illegible]	-6.991,32	-4.840,79	-1.103,9[illegible]	-306,00	-3.884,07	-3.303,00	-3.184,77	-344,81	0,00	0,00	0,00	[illegible]
compr marker mech_as ma	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
comprehensive marker matching	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
CRC_PM	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Device	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
DMH	-6.716,67	-9.753,67	-9.982,87	-11.711,67	-13.582,67	-12.886,87	-20.769,17	-17.068,87	-31.837,17	-31.844,87	-[illegible]	-15.871,17	-183.[illegible]
dummy	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Endometriosis	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
EpiLMG	-3.777,00	-3.143,00	-3.328,00	-3.063,00	-3.329,00	-1.430,00	-1.894,00	-1.818,00	-1.818,00	-1.818,00	-1.818,00	-1.818,00	-27.384,00
episcape	-3.688,00	-3.688,00	-3.688,00	-879,00	-879,00	-879,94	-1.014,90	-2.338,71	-2.338,71	-34,39	0,00	0,00	-18.194,[illegible]
EU_breast	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
PulsDxTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
HEP	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ILD	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
internal POs_before_food	-33.050,00	-8.413,00	-4.531,10	-40.413,00	-31.873,00	-79.120,00	-32.573,00	-3.331,00	0,00	0,00	0,00	0,00	[illegible]
LDI_CRC	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
marker matching improvement (PulsTech)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
MeGT_Bern	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
MeGT_validation	-9.630,83	-8.290,89	-4.909,77	-8.111,77	-7.005,01	-7.982,84	-8.194,47	-6.476,53	-4.476,53	-4.329,21	-4.329,21	-4.329,21	[illegible]
methylB-ally	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
mRNA	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Mastercells	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
NHL_Screen	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
paracrine_tech_food	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
POs_new_drug	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Preselampels	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
PT_platform (alpha assay)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Ola_deal	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_BCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Bladder_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_overhead_project_budget_AG	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Project_Managementshc	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Prostate_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Prostate_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_TAM	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Research2Assay	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ReServ	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SampleDB	-8.501,00	-3.929,00	-8.653,08	-3.413,00	-3.307,00	-3.858,70	-3.101,00	-1.212,00	-1.818,00	-1.432,8[illegible]	-1.212,00	-1.212,00	[illegible]
SampleTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Sensitive_Detection	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SeqInp	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
targeted_marker	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
VPA test & cell lines	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
xenograft	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
allocation rest operative OC (not IT)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Total Projects (direct)	-73.987,4[illegible]	-58.436,5[illegible]	-63.505,4[illegible]	-88.777,[illegible]	-88.848,[illegible]	-129.998,47	-103.738,76	-84.613,[illegible]	-[illegible],71	-61.178,11	-44.123,[illegible]	-41.[illegible]	[illegible]
Total Projects (allocation)	-41.437,[illegible]	-26.827,[illegible]	[illegible]	-34.227,87	-28.911,[illegible]	-41.849,81	-44.081,87	-47.473,[illegible]	-28.148,61	-31.321,17	-23.863,[illegible]	[illegible]	[illegible]
Total Projects	-115.184,74	-78.263,77	-91.888,80	-130.808,8[illegible]	-94.487,82	-179.708,84	-147.797,87	-91.888,3[illegible]	-88.229,11	-103.427,8[illegible]	-101.087,81	-122.228,8[illegible]	-1.221.430,87
Total OC	-39.630,87	-46.728,08	-38.303,81	-38.835,87	-32.889,87	-43.821,3[illegible]	-48.883,87	-38.329,[illegible]	-47.891,27	-44.037,[illegible]	-43.943,81	-48.431,87	-473.571,[illegible]
BizDev													
Total	-63.798,[illegible]	-64.643,[illegible]	-60.638,81	-63.288,83	-65.717,[illegible]	-66.472,[illegible]	-78.988,87	-64.071,11	-60.883,77	-64.389,[illegible]	-61.778,33	[illegible]	-739.[illegible]
Admin													
Total	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
profit/loss	-111.873,9[illegible]	-74.895,13	-191.183,81	-114.322,53	-171.390,81	-214.631,8[illegible]	-447.173,0[illegible]	-65.346,4[illegible]	-114.125,4[illegible]	-136.[illegible]	347.877,8[illegible]	-320.796,[illegible]	-1.086.164,5[illegible]

C	Central R&D Budget 2004												
	Jan. 04	Feb. 04	Mrz. 04	Apr. 04	Mai. 04	Jun. 04	Jul. 04	Aug. 04	Sep. 04	Okt. 04	Nov. 04	Dez. 04	Total 2004
REV	43.638,40	43.638,40	43.638,40	19.891,72	19.891,72	29.891,72	146.198,40	146.198,40	171.198,40	146.198,40	146.198,40	152.898,17	1.097.861,84
COGS													
alleles													
allelotyping	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AmpliTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AmpliTech_RAbleTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AssayDesign	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
autolabeling	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BioTools	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Bisulfite_Bis_Replacing_Techn	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Bisulfite_Bis_Replacing_Techn_Design	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
biwLW	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BOCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
cell_diag_tech_feas	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Chipping	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
compr marker mech_m ma	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
comprehensive marker machine	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
CRC_Pal	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Device	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
DMH	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
dummy	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Endometriosis	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
EpiLMG	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
episcope	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
EU_breast	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
RAbleDxTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
HTP	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ILD	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
internal PDs_before_feas	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
LDI_CRC	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
marker maching improvement (RAbleTech)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
MGST_Bone	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
MGST_validation	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
methylLight	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
mRNA	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Microarray	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
NHL_Screen	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
paraffin_tech_feas	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
PDs_new_drug	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Prostatepals	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
PT_platform_(alpha score)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Ola_diag	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_BCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Bladder_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_overhead_project_budget_AG	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Project_Management	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Prostate_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Prostate_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_TAM	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ResearchAssays	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ReSeq	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SampleDB	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SampleTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Sensitive_Detection	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Sequencing	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
transcription_marker	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
VPA test & cell lines	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
xenograft	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
allocation opex operating CC (incl IT)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Total Projects (direct)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Total Projects (allocation)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Total Projects	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
gross margin	43.638,40	43.638,40	43.638,40	19.891,72	19.891,72	29.891,72	146.198,40	146.198,40	171.198,40	146.198,40	146.198,40	152.898,17	1.097.861,84
R&D													
alleles													
allelotyping	0,00	0,00	-3.346,87	-4.074,07	-4.866,71	-4.336,43	-4.866,71	-4.706,13	-7.712,43	-4.000,89	-4.050,89	-4.874,42	[illegible]
AmpliTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
AmpliTech_RAbleTech	-1.717,60	-1.302,24	-1.537,00	-1.242,74	-3.302,77	-3.302,77	-4.575,86	-4.815,76	-4.611,72	-4.313,46	-4.784,00	-4.784,00	-44.[illegible],00
AssayDesign	-8.434,00	-1.818,00	-3.121,00	-1.818,00	-2.121,00	-4.061,28	-2.121,00	-2.121,00	-2.843,00	-2.121,00	-3.424,00	-4.835,87	-38.444,80
autolabeling	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BioTools	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Bisulfite_Bis_Replacing_Techn	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Bisulfite_Bis_Replacing_Techn_Design	-7.053,00	-4.918,00	-10.044,80	-4.017,00	-4.127,00	-4.127,00	-4.470,00	-11.615,77	-7.809,43	-4.[illegible],11	-7.584,21	-7.224,00	-104.[illegible]
biwLW	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
BOCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
cell_diag_tech_feas	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Chipping	-4.729,89	-12.874,25	-4.543,00	-10.807,81	-4.236,00	-7.343,83	-13.209,00	-11.857,58	-14.150,33	-4.446,00	-4.600,00	-4.800,00	-125.887,22
compr marker mech_R_PA	-3.800,00	-7.433,00	-21.784,00	-12.171,00	-14.434,00	-18.807,00	-30.804,00	-21.038,00	-32.431,00	-44.301,00	-72.154,00	-20.808,00	-308.113,80
comprehensive marker machine	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
CRC_Pal	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Device	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
DMH	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
dummy	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Endometriosis	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
EpiLMG	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
episcope	-3.544,00	-3.546,00	-3.546,00	-479,00	-479,00	-479,84	-1.814,86	-4.334,71	-4.334,71	0,00	0,00	0,00	-18.[illegible]
EU_breast	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
RAbleDxTech	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
HTP	-118.838,17	-134.874,17	-143.162,17	-130.724,17	-158.745,17	-60.728,17	-79.813,17	-170.629,17	-132.559,17	-123.884,17	-114.885,17	-43.173,17	-1.384.137,[illegible]
ILD	-4.184,00	-3.846,00	-8.711,83	-3.794,87	-7.114,87	-7.114,87	-7.114,87	-7.114,87	-3.794,87	-3.794,87	-4.794,87	-3.804,87	-62.679,[illegible]
internal PDs_before_feas	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
LDI_CRC	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
marker maching improvement (RAbleTech)	-14.120,00	-14.120,00	-13.804,00	-13.348,00	-17.808,00	-18.880,00	-19.879,00	-30.779,00	-33.771,00	-30.808,00	-30.108,00	-17.199,00	[illegible]
MGST_Bone	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
MGST_validation	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
methylLight	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
mRNA	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Microarray	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
NHL_Screen	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
paraffin_tech_feas	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
PDs_new_drug	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Prostatepals	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
PT_platform_(alpha score)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Ola_diag	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_BCS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Bladder_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Colon_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_overhead_project_budget_AG	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Project_Management	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Prostate_Cancer_MCT	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_Prostate_CS	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
R_TAM	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ResearchAssays	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
ReSeq	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SampleDB	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
SampleTech	-4.547,00	-7.440,00	-16.772,00	[illegible]	[illegible]	-20.983,00	-4.003,00	-4.803,00	-40.423,00	-13.812,00	-10.831,00	-7.344,00	-132.[illegible]
Sensitive_Detection	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Sequencing	-7.338,00	-21.380,00	-13.073,00	-16.043,00	-4.630,00	-4.448,00	0,00	0,00	0,00	0,00	0,00	0,00	-67.[illegible]
transcription_marker	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
VPA test & cell lines	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
xenograft	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
allocation opex operating CC (incl IT)	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
0	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Total Projects (direct)	-183.314,[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-144.[illegible]	-195.135,[illegible]	[illegible]	[illegible]	[illegible]	-189.407,[illegible]	-180.097,77	[illegible]
Total Projects (allocated)	-72.573,[illegible]	-58.429,15	-57.279,84	[illegible]	-48.884,17	-96.223,[illegible]	-81.777,71	[illegible]	15.[illegible]	-81.344,71	-60.[illegible]	-170.[illegible]	[illegible]
Total Projects	-384.887,17	-471.477,62	-412.401,10	-443.176,[illegible]	-478.843,[illegible]	-398.896,41	-476.972,[illegible]	-419.841,48	-488.399,57	-474.624,[illegible]	-[illegible]	-[illegible]	-[illegible],41
Total CC	-149.788,81	-138.948,14	[illegible]	-138.138,[illegible]	-171.873,49	-177.484,[illegible]	-171.887,[illegible]	-139.447,79	-178.[illegible],79	[illegible]	-199.404,76	-[illegible],110,[illegible]	[illegible]
BizDev													
Total	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
Admin													
Total	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00
profit loss	-490.438,86	-394.844,37	-437.988,81	-491.773,81	-439.340,86	-948.461,37	-473.132,17	-480.098,00	[illegible]	-473.702,[illegible]	-412.918,87	-496.799,[illegible]	-4.[illegible]